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July 19, 2006, 06:49:14; Search time 4394 Seconds (without alignments) 10187.345 Million cell updates/sec
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1 ctgtttcacataaagttttt........gccttttaggtgatgtggca 700
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 70 summaries
                                                                 OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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SUMMARIES			Ω	AC006344	AC167793		AC007276	AC011079	AC025490	AC093671			~				AC110584		AC016756	AC090150	AC008022
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	ф	Query	Match	8.66	24.0	16.5	16.5	16.5	16.5	16.5	16.5	16.3	16.3	16.3	16.2	16.2	16.1	16.1	16.1	16.1	16.0
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AC055 BV184 BV612 BV612 BV612 BV612 AC012 AC0092 AC092 AC092 AC092 AC092 AC092 AC092	AC0535 AC0535 AC0535 AC0535 AC01048 BV63942 BV63942 AC01083 AC1083 AC1083 AC1083 AC1083	AP001034 AC107538 AC153174 AC153174 AC07205, AC07205, AC125629 AC125629 BV6411917 AC100647, AC01797	AC008400 2 AC14158 AC09410 AC009410 AC00948 AC02235 2 AC079942 2 AC079942 2 AC079942 2 AC079942 AC079943 AC079943
6.0 16678 6.0 18372 6.0 18614 5.9 60 5.9 75 5.8 18230 5.8 18230 5.8 17318 5.8 17318 5.8 17318	55.7 18129 55.7 18129 55.7 18129 55.7 20321 55.7 20321 73.8 2033 56.7 85832 57.8 85832 57.8 85832 57.8 85832 57.8 85832	15.6 167934 15.6 178544 15.6 178544 15.6 141147 15.6 181557 15.5 181557 15.5 1870427 15.5 1870427 15.5 1870427 15.5 1870427 15.5 1870427 15.4 38837 15.4 38837	5.4 11740 5.4 117180 5.4 10981 5.4 20043 5.4 20043 5.4 20043 5.3 11000 5.3 11000 5.3 13955
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## ALIGNMENTS

	Homo sapiens PAC clone RP4-726N20 from 7g32-g34, complete sequence. AC006344 AC06344.2 GI:4508150 HTG. saniens (Muman)		1 (bases 1 to 127447) Sulston,J.E. and Waterston,R. Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
RESULT 1 AC006344/c LOCUS	DEFINITION HACCESSION PACESSION PACESSION PACESMONDS HACCESTON PACES PAC	MSIR	REFERENCE 1 AUTHORS S TITLE 1 JOURNAL G

no read

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                                              The run of A's from 48936 to 48936 may contain one less A, was able to make an exact call.
Location/Qualifiers
1. .127447
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3754. 4007
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of RP4-726N20.
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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VECTOR: pCYPAC2
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP4-529P3. Actual start of this
clone is at base position 1 of RP4-726N20; actual end is at 127447
                                                                                                                                                                                   Submitted (11-JAN-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 4 (bases 1 to 127447) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 24, 1999 this sequence version replaced gi:4139379.
                                                                                                                                                                                                                                                                                                                                        Submitted (24-MAR-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 5 (bases 1 to 127447) Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (10-701-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
6 (bases 1 to 127447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 00); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted:
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                       2 (bases 1 to 127447)
Cordes,M., Wohldman,P., Pape,K. and Hotic,M.
The sequence of Homo sapiens PAC clone RP4-726N20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: WVGSC
                                                                                                                     3 (bases 1 to 127447)
Waterston, R.H.
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Qy         421 TAATTGATTTTACCAAATTTCCATGGAACAAGG           Db         95109 TAATTGATTTTACCAAATTTCCATGGAACAAGGAGG           Qy         481 TTTGAAATACTAGTACGGAATATCATTGTTAGTTGA	541 541 94989	Qy 601 TATGATAATTAGTGAAACACCCAAGAATGTTTATA	Qy 661 TGACACTTGGAGTAACAATTGCCTTTTAGGTGATGTG	RESULT 2 AC167793/C LOCUS DEFINITION Bos taurus clone CH240-216G5, WORKING D		_	REFERENCE 1 (bases 1 to 197215) AUTHORS Muzny,D., Adams,C., Agbai II,O., Allen, Arredondo,H., Bandaranaike,D., Bangura, Beraducci,A., Biswalo,K., Blyth,P., Bon Cadoree,I., Canada,A., Cardenas,V., Car	Cheng, M1., Chu, J., Clerc, K., Cockrell Curar, S. Dai, M., Davila, M.L., Davis, C. Anda, C., Delgado, O., Denson, S., Donlin, J., McCauley, S., Dugan-Rocha, S.,	Fernada, D., Egan, A., Escotto, M., Espinos Fernadaca, S., Fernando, P., Flagg, N., Fo Fowler, G., Fu.C., Fuh, E., Garcia, A., Ga Gaskin, C., Gench, S., Ghose, S., Gill, R.,	GOTZAIEZ-CATAY, M., GUEVATA, W., HOLGEY, M., HOLGEY, M., HAMILON, K., HATDES, HAWKINS, E., HAYES, S., HEMPHILI HAWES, S., HICCHENS, M., HOGGSON, A., HOGU	JACOBLI, I.I., HULYK, S., HUNE, J. INC., K., JACOB, L., Jang, H., Johnson, B., Johnson, Keys, T., Khan, Z., King, L., Kovar, C., Kora, S., Lecal, S., Leca	London, P., Lopez, J., Lorensuhewa, L., Maheshwari, M., Mahoney, C., Malloy, K., Malloy, K., Mclelland, H., McPherson, J., Mercadao, C., Malloy, M., McMarson, J., Mercadao, C., Malloy, M., McMarson, M., Mercadao, C., Malloy, M., Mercadao, C., Malloy, M., Mercadao, C., Marcadao, C., Marcadao, C., Marcadao, C., Mercadao, C., Mercada, C.,	Murray, D., Nazarith, L., Ngo, D., Nott, A., Nwaokelemeh, O., Obregon, M., Ocokwoonu, G., Okwoonu, G., Okwoonu, G., Oswoonu, G., Oswoonu, G., Oswoonu, G., Oswoonu, G., Oswoonu, G., Oswoonu, G., Parker, D., Past	Primus, E., PuinI., Puazo, M., Qin, X., Rabata, D., Rachlin, E., Reigh, R., Ren, Y. Raves, C., Rodriguez, F., Rojas, A., Ruiz, C., Rodriguez, P., Rojas, A., Ruiz, C., Rodriguez, P., Rojas, A., Ruiz, C., Ruiz,	Signature, Sancol, Sancol, Savery, S. Song Svatek, A., Taylor, E., Taylor, T., Thomas Trejos, Z., Usmani, K., Vargo, C., Verduzc Volkov, A., Waldron, L., Walker, B., Wang,
repeat_region 55105572  repeat_region 57145738  repeat_region 57396032  repeat_region 57396032  repeat_region 57396032	Type family="AT_rich"	eature	misc_reature 6362649U //gene="WUGSC:H_DJ0726N20.1" //note="match to EST R62790 (NID:g834669) yil0h10.r1" misc_feature 63626490		misc_feature 63786490 /gene="WUGSC:H_DJ0726N20.1" /note="match to EST T23736 (NID:g519976)" misc_feature 6383640 DJ0726N20.1"	/note="match to EST H06508 (NID:g870040) y178e08.s1" repeat_region 69797247 /rpt_family="Alu" misc_feature 75237578	/gene="WUGSC:H_DJ0726N20.1" /note="match to_EST_AA741361 (NID:g2779953) ny96e04.s1" /note="match to_EST_AA741361 (NID:g3779953) ny96e04.s1" /gene="WUGSC:H_DJ0726N20.1" /note="match to_EST_AA974551 (NID:g3149731) oo92h08.s1" misc_feature 75247578	Query Match 99.8%; Score 698.4; DB 5; Length 127447; Best Local Similarity 99.9%; Pred. No. 6.1e-194; Matches 699; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Oy 1 CIGITICACAIDAAGITITITITITITAAGAATITIAAAAAAATAICAITITITITITITI 60 	OY 61 ATTATTATTATACTTTTAAGTTTTAGGGTACATGTGCAAAGTGTGCAGGTTAGTTA	Qy 121 TATATACATGTGCCATGCTGGTGTGCTGCACCATTAACTCACATGAAGTTTTTTTAAA 180	QY 181 ITTTAGTGACAGTTTTAGTCATTTTCCTAATTGAAGTATCATAAGTAATCCATAAATTT 240	Oy 241 GAAAAAATGTTAACTACTCTGATAAAAAAGTTTTATAGTTTCCTACTTTTAAGCAAAAT 300 	Qy 301 TCCATAGGGCATGGTAATTGTAGTTTCAACATTACTTGCAGTTTCAGTTAGTAAATAAA	Qy 361 ATTAAGCTAGTAATATTTAATATTGTCAAATAATTTGGAAAATACCATGGGTACT 420 

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len,C., Alsbrooks,S., Archer,P.,
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GGTTGGCTATTTTTGGATTGATAT 480
                                                                                                                                                        A linear HTG 23-JAN-2006
DRAFT SEQUENCE, 8 unordered
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etartiodactyla; Ruminantia;
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|GGCA 94830
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The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using ALIas and whole genome shotgun sequencing reads assembled using ALIas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contigs scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Wei, X., Wheeler, D., Williams, G., Williams, R., Worley, K., Wright, R., Wu, J., Yakub, S., Yan, K., Yuan, Y., Yu, F., Zhang, J., Zhang, L., Zhang, Z., Zhou, J., Weinstock, G. and Gibbs, R.A. Direct Submission
                                                                                                                                                         Direct Submission
Submitted (04-SEP-2005) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 197215)
                                                                                                                                                                                                                                                                                                                                Submitted (23-JAN-2006) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: Atlas 3.0;
Consensus quality: 193754 bases at least Q40
Consensus quality: 194610 bases at least Q30
Consensus quality: 195146 bases at least Q20
Estimated insert size: 195308; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of 50 bp

contig of 20861 bp in length

contig of 22353 bp in length

gap of 70 bp

contig of 122800 bp in length

gap of 80 bp

contig of 9904 bp in length

contig of 9904 bp in length

contig of 15508 bp in length

contig of 15508 bp in length

contig of 15508 bp in length

gap of 60 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195958: contig of inknown length
195958: contig of 1364 bp in length
59 195958: gap of unknown length
59 197215: contig of 1257 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig of 1637 bp in length
gap of 50 bp
contig of 20861 bp in length
gap of 779 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Baylor College of Medicine
Center code: BCM
                                                                                                                                                                                                                                                                                          Bovine Genome Sequencing Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----- Genome Center
                                                                                                                (bases 1 to 197215)
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168882:
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                                                                                            Unpublished
                                                                                                                                       Worley, K.C.
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195959
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AUTHORS
CONSRTM
TITLE
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COMMENT

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143345 ATGGATTTGAAGGGAAGTGTTAAATACTCTGATAAAGAAGTTTGCAGTTTTC---TATTTC 143289
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Homo sapiens chromosome RPCI-11 clone RP11-707H2, WORKING DRAFT
SEQUENCE, 7 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143403 TGTTTCATATAAGTTTTTTTTAAATATTTTTTTAAGTAAAGCA--ATAAGTGATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143239 GAATGCATC------TAATTTAGTTTTGCTAAATAGCTAGGAAATATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 ATAAATTTGAAAAAATGTTAACTACTCTGATAAAAAGTTTTATAGTTTTCCTACTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 AAATAAATATTAAGCCTAGTAAAGTATAATTTTAATATTGTCAAATAATTTGGAAAATACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  573 TGATTTAATAATGGTATGGAGTTAGGGCTATGATAATTAGTGAAAACACCCCAAGAATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 AGCAAAATTCCATAGGGCATGGTAATTGTAGTTTCAACATTACTTGCAGTTTCAGTTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GGATTGATATTTTGAAATACTAGTACAGGAATATCATTGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 197215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 120; Indels
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168883. .168932
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Best Local Similarity 67.2%;
Matches 371; Conservative
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PRI 08-OCT-2003
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Waterston, R.H.
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5. (bases 1 to 172573)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Homo sapiens BAC clone RP11-22601 from 7, complete sequence.
AC007276
                                                                                                                                                                                                                                                                                                                                                                 DB 12; Length 159859;
                                                                                                                                                                                                                                                                                                                                                               Score 115.6; DB 12; Length
Pred. No. 1.5e-23;
0; Mismatches 19; Indels
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Joshu, C., Le, T., Maupin, R. and Yoakum, M.
The sequence of Homo sapiens BAC clone RP11-22601
Unpublished (2001)
                                                                              J2314. .50864
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50865. .50964
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/note="assembly_name:Contigl2"
                                                                                                                                                                                                                                                                         /estimated length=unknown
107063. .159859
/note="assembly_name:Contig14"
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1 (bases 1 to 172573)

Sulston, J.E. and Wilson, R.

Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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16170. .32213
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74132. 106562
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106963. 107062
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                                                       32214. .32313
/estimated_length=unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 TGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                           74032. .74131
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Waterston, R.H.
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87.0%;
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Matches 127; Conservative
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Best Local
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ACCESSION
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                                                                                                                                                                                                    Direct Submission
Submitted (09-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Aug 21, 2000 this sequence version replaced gi:9857594.
                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                    Center: Washington University Genome Sequencing Center
Center code: WUGSC
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app of unknown length
contig of 52797 bp in length.
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mol_type="genomic DNA"
db_xref="texon:9606"
/chromosome="RPC1-1"
/clone="RP11-707H2"
                                                                                                                            The sequence of Homo sapiens clone
Unpublished
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 HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                   Hominidae, Homo.
1 (bases 1 to 159859)
Waterston, R.H.
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Waterston, R.H.
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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Exic D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University denome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov or see http://genome.wustl.edu
  Direct Submission
Submitted (29-APR-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
7 (bases 1 to 172573)
Wilson,R.
                                                                                                                                                                                                                                                                                                        Submitted (08-OCT-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Dec 16, 1999 this sequence version replaced gi:5001518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTICE: This sequence may not represent the entire insert of this folone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 0); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
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The clone sequenced to the right is RP11-332C7, 200 bp overlap.
Actual start of this clone is at base position 1 of RP11-22601 actual end is at base position 172379 of RP11-22601.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://genome.wustl.edu
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
Center project name: H.NH0226001
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/db_xref="taxon:9606"
/chromosome="7"
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/clone_lib="RPCI-11"
1. .161
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/rpt_family="MaLR"
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170. .282
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6591. .6658 /rpt\_family="MER1\_type" 6662. .7326

J381. .5673 /rpt\_family="Alu" 6591. .6650

/rpt\_family="Alu" 5381. .5673

rpt\_family="GA-rich"

/rpt\_family="L1" 7330. .7476

'rpt\_family="ERVL" 0220. .10513

rpt\_family="Alu" rpt\_family="MIR"

rpt\_family="MIR"

.9031

. .10513 family="Alu"

rpt\_family="MaLR" 2272. .12560

.12560 12592

family="Alu"

rpt\_f 2561.

family="MaLR"

/rpt\_fami 11924. .13 rpt\_f2 1586. rpt\_f 10797.

family="Alu"

rpt\_f 217<u>5</u>.

family="Alu"

.11140

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FEATURES

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Center project name: 45.112

Center project name: 45.112

Center clone name: 45.112

Center clone name: 45.112

Sequencing vector: M13, M7815; 50% of reads
Sequencing vector: Plasmid; n/a; 50% of reads
Chemistry: Dye-primer-amersham; 2% of reads
Chemistry: Dye-terminator Big Dye; 9% of reads
Chemistry: Dye-terminator Big Dye; 9% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 146316 bases at least Q40
Consensus quality: 147173 bases at least Q30
Consensus quality: 147173 bases at least Q20
Insert size: 142000; agarose-fp
Insert size: 142000; agarose-fp
Insert size: 147559; sum-of-contigs
Quality coverage: 11.4 in Q20 bases.
**NOTE: This is a "working draft' sequence. It currently
consists of 4 contigs. The true order of the pieces
**is not known and their order in this sequence record is
**is not known and pheir order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 28597: contig of 28597 bp in length 28598 286598 286599 app of 100 bp 77951 77950: contig of 49253 bp in length 77951 28050: gap of 100 bp 78051 129173: contig of 51122 bp in length 129773 129272: gap of 100 bp 129273 147859: contig of 18587 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 16.5%; Score 115.2; DB 12; Length Best Local Similarity 87.5%; Pred. No. 2e-23; Matches 126; Conservative 0; Mismatches 18; Indels
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                                                                                                                                    Center code: WIBR
Web site: http://www-seg.wi.mit.edu
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|db xref="taxon:9606"
|clone="RP11-45112"
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1. .147859
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vector_side:left"
28598. . . 28697
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                    COMMENT
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Submitted (01-OCT-1999) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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87.0%; Pred. No. 1.5e-23;
live 0; Mismatches 19;
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AC011079.3 GI:11136801
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Matches 127; Conserv
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                    repeat_region
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DEFINITION
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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REFERENCE
AUTHORS
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NOTE: This is a 'working draft' sequence. It currently consists of 12 contigg. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Insert size: 168721; sum-of-contigs
Quality coverage: 5.0 in Q20 bases; agarose-fp
Quality coverage: 4.8 in Q20 bases; sum-of-contigs
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4: contig of 2255 bp in length
4: gap of 100 bp
6: contig of 8184 bp in length
7: gap of 100 bp
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gap of 100 bp
contig of 33598 bp in length.
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gap of 100 bp
contig of 92 bp in length
gap of 100 bp
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vector_side:right"
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  89926 AAGTTTTAGGGTACATGAGCACAATATGCAGGTTAGTTACATATGTATACATGTGCCATG 89985
                                                                                                                                                                                                                                                     169821 bp DNA linear HTG 28-MAR-2000
Homo sapiens chromosome 4 clone RP11-6901 map 4, WORKING DRAFT
SEQUENCE, 12 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (199-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 28, 2000 this sequence version replaced gi:7212073. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Center: Whitehead Institute/ MIT Center for Genome Research
                                            Center clone name: 62-01

Sequencing vector: M13; W77815; 100% of reads
Sequencing vector: M13; W77815; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 163347 bases at least Q40
Consensus quality: 167964 bases at least Q30
Consensus quality: 167961 bases at least Q30
Insert size: 163000; agarose-fp
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1 (bases 1 to 16921)

1 "theres 1 to 16921)

1 "thren, B. Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 4, clone RP11-6901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www-seg.wi.mit.edu
                                                                                                                                                    89986 CTGGTATGCTGCACCCACTATCTC 90009
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                                                                                                                                CTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                     HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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AC025490.2 GI:7331510
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                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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AC025490
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100 bp of 15698 bp in length 100 bp

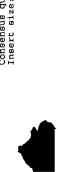
100 bp of 8160 bp in length 100 bp of 9953 bp in length 19447 bp in length

18079 bp in length

100 bp

in length

100 bp of 26767 bp 100 bp



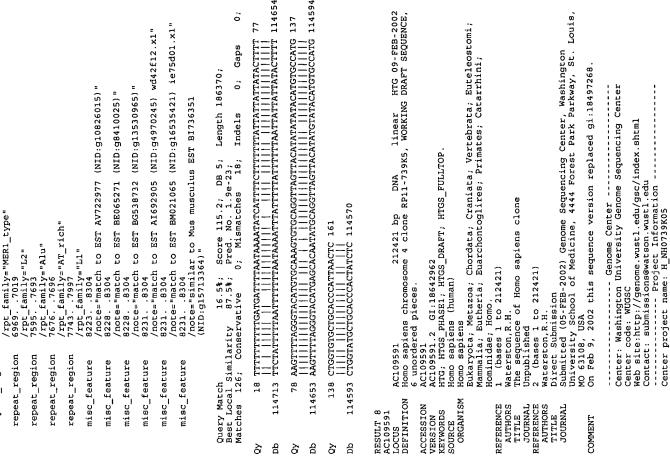
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC093671 10-JAN-2002
Homo sapiens BAC clone RP11-542P2 from 4, complete sequence.
AC093671
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Direct Submission
Submitted (07-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
M 0 53108, USA
4 (bases 1 to 186370)
Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (15-DEC-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                         18 TITITITITIGATGATTITIAATAAAATATCATTITITITITITITITATTATATATCTTTT
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Holmes, A., Elliott, G. and Kozlowicz, A.
The sequence of Homo sapiens BAC clone RP11-542P2
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                         18;
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Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                       16.5%; Score 115.2; DB
87.5%; Pred. No. 2e-23;
ative 0; Mismatches 1
                                                                                                                                                                                                       111453. .111552
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| 136124. .136223
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                                                                                                                                                                                                                                                                                        estimated_length=100
estimated_length=100
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Sulston, J.E. and Waterston, R.
                                                                                                             clone_end:T7 __
vector_side:right"
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                                               65039
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Waterston, R.
Direct Submission
Submitted (10-JAN-2002) Department of Genetics, Washington
Submitted (10-JAN-2002) Avenue, St. Louis, Missouri 63108, USA
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Dec 15, 2001 this sequence version replaced gi:16259163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Morpherson, Department of Genetics, Washington University, St. Louis
MCP. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P. Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J. J. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and Coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The clone sequenced to the left is AC048378; the clone sequenced to the right is RP11-5X16. Actual start of this clone is at base position 1 of RP11-542P2; actual end is at base position 186370 of
                               Waterston, R.H.
Direct Submission
Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 186370)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="match to EST BM021296 (NID:g16535652) ie75d01.y1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: H_NH0542P02
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1. .186370
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db & xref="taxon:9606"
/chromosome="4"
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NEIGHBORING SEQUENCE INFORMATION:
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/clone_lib="RPCI-11"
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/rpt_family="Alu"
4. .22
(bases 1 to 186370)
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Waterston, R.H.
The sequence of Homo sapiens clone
Unpublished
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                                                                         /o/6..7696
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7743..7997
/rpt_family="L1"
8223..8304
5552. .5650
/rpt_family="MER1_type"
6969. .7019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 CTGGTGTGCTGCACCCATTAACTC 161
                                           /rpt_family="L2"
7595. .7693
/rpt_family="Alu"
7676. .7696
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1 (bases 1 to 212421)
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AC109591
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 'note="match to EST BG940813 (NID:g14340185) ax07g01.rl"
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5107. .5293
/note="match to EST AA909866 (NID:g3049156) ol09h06.s1"
                                                                                                                                                                                                                                                                                                          (NID:93678721) qf34f05.x1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="match to EST AW469038 (NID:g7039144) hd30g07.x1"
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/note="match to EST BG613633 (NID:g13665004)"

/note="match to EST BG477315 (NID:g13409594)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="match to EST BG388087 (NID:g13281533)"
2747. .2829
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2763. .2829
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/note="match to EST BG707099 (NID:g13983105)"
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note="match to EST BI760964 (NID:g15752542)"
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Ancte="similar to Homo sapiens BST BI547286
(NID:915434598)"
                               note="match to EST AW137642 (NID:g6141960)'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="similar to Homo sapiens EST BI547286 (NID:g15434598)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="similar to Homo sapiens EST BE567541
                                                                                                                             Homo sapiens EST BE961990
                                                                                                                                                                                                                                                                                                        'note="match to EST Al150252
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/rpt_family="L1"
2190. .2192
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note="match to EST
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4143. 4157
                                                                                                                          'note="similar to
(NID:g11764436)"
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4393. 4623
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/rpt_family="MIR"
4804. .5293
                                             479. .613
/rpt_family="L1"
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1392. .1412
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/rpt_family="L1"
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              Sequencing vector: M13, 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 20891 bases at least Q40
Consensus quality: 210714 bases at least Q30
Consensus quality: 211269 bases at least Q20
Insert size: 190000; agarose-fp
Insert size: 212031; sum-of-contigs
Quality coverage: 6.42 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4750: contig of 4750 bp in length
4850: gap of unknown length
39482: contig of 34632 bp in length
35829: gap of unknown length
68572: contig of 28990 bp in length
68725: gap of unknown length
92735: contig of 24063 bp in length
92735: contig of 24063 bp in length
131161: contig of 38282 bp in length
131261: gap of unknown length
131261: gap of unknown length
212421: contig of 81160 bp in length
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/estimated_length=unknown
4851. .39482
/note="assembly_name:Contig14"
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/estimated length=unknown
39583. .68572
/note="assembly_name:Contig15"
68573. .68672
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/note="assembly_name:Contig13"
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58673. .92735
/note="assembly_name:Contigl6"
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92836. .131161
/note=rassembly_name:Contig17"
131162. .131261
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----- Summary Statistics

    212421
    organism="Homo sapiens"

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/db_xref="taxon:9606"
/chromosome="4"
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Similarity

Matches 126;

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17

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Hominidae, Pan.

Is (bases 1 to 161343)

Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W. Bouffard,G.G., Brinkley,C., Brooks,S., Cariaga,K.,
Chu,G., Coleman,B., Coleman,H., Engle,J., Granite,S., Guan,X.,
Gupta,J., Haghighi,P., Han,J., Hansen,M., Ho,S.-L., Hu,P.,
Hurle,B., Idol,J.R., Karlins,E., Kwong,N., Laric,P., Lee-Lin,S.-Q.,
Legaspi,R., Maduro,Q.L., Maduro,V.B., Margulies,E.H., Masiello,C.,
Maskeri,B., McDowell,J., Paguirigan,C., Pearson,R., Portnoy,M.E.,
Prasad,A., Reddix-Dugue,N., Schandler,K., Schueler,M.G., Shah,K.,
Sison,C., Stantripop,S., Thomas,J.W., Thomas,P.J., Tsipouri,V.,
Vogt,J.L., Wetherby,K.D., Wiggins,L., Young,A. and Green,E.D.
                                 93460 AAGTTTTAGGGTACATGAGCACAATATGCAGGTTAGTTACATATGTATACATGTGCCATG 93519
                                                                                                                                                                                                                                                                                                                                             AC144869 161343 bp DNA linear HTG 09-JUN-2003
Pan troglodytes clone CH251-287A2, WORKING DRAFT SEQUENCE, 7
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 160248 bases at least Q40
Consensus quality: 160266 bases at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (23-MAY-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 161343)
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Web site: http://www.nisc.nih.gov
Contact: nisc zoo@nhgri.nih.gov
                                                                                                                                                     93520 CTGGTATGCTGCACCCACTATCTC 93543
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Center clone name: 287A02
                                                                                                                       138 CTGGTGTGCTGCACCCATTAACTC 161
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Pan troglodytes (chimpanzee)
Pan troglodytes
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Direct Submission
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
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JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
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KEYWORDS
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• consists of 7 configs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

25269 25368; contig of 5268 bp in length 25369 40449; contig of 15081 bp in length 4650; contig of 1377 bp in length 40550 4049; contig of 1377 bp in length 40550 contig of 7471 bp in length 40550 contig of 1471 bp in length 40550 contig of unknown length 40550 contig of unknown length 40550 contig of 1471 bp in length 40550 contig of unknown length 40550 contig of 1471 bp in length 55498 55597; contig of 16830 bp in length 95597; capt of unknown length 95598 6527; gap of unknown length 95598 6527; gap of unknown length 95598 6527; gap of unknown length 95598 9557; gap of unknown length
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                    Insert size: 178000; agarose-fp
Insert size: 160743; sum-of-contigs
Quality coverage: 10.74x in Q20 bases; agarose-fp
Quality coverage: 11.89x in Q20 bases; sum-of-contigs
                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96210: contig of 3683 bp in length
96310: gap of unknown length
161343: contig of 65033 bp in length.
Consensus quality: 160675 bases at least Q20
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/organism="Pan troglodytes"
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48027. .55497
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25369. 40449
/note="assembly_fragment"
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/estimated_length=unknown
92528. .96210
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96311. .161343
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/note="assembly_fragment"
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/db xref="taxon:9598"
/clone="CH251-287A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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vector_side:left"
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96210:
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clone_end:SP6
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Score 114.4; DB 12; Length 161343; Pred. No. 3.4e-23; 0; Mismatches 26; Indels 0; G

16.3%; illarity 83.3%; Conservative

Query Match Best Local Similarity Matches 130; Conserv

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PRI 09-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Direct Submission
Submitted (12-ULL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
5 (bases 1 to 135692)
                                                                                                                                                                                                                                                                                                                       ACO21134 135692 bp DNA linear PRI 09-JJ
Homo sapiens BAC clone RP11-402D23 from 4, complete sequence
ACO21134
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On Jul 12, 2001 this sequence version replaced gi:14573744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
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Center code: WUGSC
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                                                                                                                      126 ACATGTGCCATGCTGGTGCTGCACCCATTAACTC 161
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Contact: sapiens@watson.wustl.edu
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Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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Waterston, R.H.
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Waterston, R.H.
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Length 135692;
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Pred. No. 4.6e-23;
                                                                                                                                                /rpt_family="MIR"
2160.21637
/rpt_family="AT_rich"
21750..21820
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/rpt_family="GA-rich"
21864..23052
/rpt_family="RV1"
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23563..23596
/rpt_family="L1"
24614..24707
/rpt_family="L2"
25286..25758
/rpt_family="ERVL"
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13053. .33255
15073. .15665
/rpt_family="ERVL"
15708. .1634
/rpt_family="ERVL"
16344. .16645
/rpt_family="L2"
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/rpt_family="C2"
/rpt_family="C2"
/rpt_family="C2"
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/rpt_family="ERVL"
26291. . 26313
/rpt_family="AT_rich"
27735. . 28061
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38145. .38167
/rpt_family="AT_rich"
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27861 .27884
/rpc family="(A)n"
28036 .28062
/rpc family="(GAA)n"
28108 .28669
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7474. 38152
rpt_family="L1"
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28898. .2930c
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/rpt_family="ERVL"
29857. .30047
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36190. .36663
/rot_family="L1"
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36826. .36956
/rpt_family="L1"
37137. .37158
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37447. .37472
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0674. .30965
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34203. .34248
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1191. .3142^
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12660. .32718
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86.7%;
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                                                                                                                                           The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and Coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
                                                Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                VECTÖR: pBACe3.6
BIGGHORING SEQUENCE INFORMATION:
The clone sequenced to the left is AC005150, 2000 bp overlap.
Actual end of this clone is at base position 135692 of RP11-402D23.
                                                                                                                                                                                                                                                                                                                                                                 Polymorphisms have been identified between AC005150 and RP11-402D23.
                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                               mol_type="genomic DNA"
(db_xref="taxon:9606"
(chromosome="4"
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2219. .2247
/rpt_family="(T)n"
4589. .4646
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clone_lib="RPCI-11"
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rpt_family="(ATG)n"
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1877. .9023
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1545. .11707
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rpt_family="ERVL"
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2. .532
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12184. 12212
/rpt_family="(A)n"
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/rpt_family="L1"
7208. .725
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1476. .11541
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rpt_family="MIR"
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family="MIR"
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                                MAPPING INFORMATION:
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Gaps
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1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Washington University Genome Sequencing Center
Center code: WUGSC
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Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: M13; 0% Sequencing vector: plasmid; 100% Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 156145 bases at least Q40 Consensus quality: 156237 bases at least Q20
                                                                                                                                                                                                                     114963 TACATGTGCCATGCTGGTGTGCTGCACCCATTAACTCA 115000
                                                                                                                                                                                                125 TACATGTGCCATGCTGGTGTGCTGCACCCATTAACTCA 162
20;
0; Mismatches
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1. 156393
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1 (bases 1 to 156393)
Waterston, R.H.
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Waterston, R.H.
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Homo sapiens
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Matches 137; Conservative
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DEFINITION
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AC116177
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KEYWORDS
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Hominidae; Homo.
Hominidae; Homo.
Hominidae; Homo.

I (bases I to 154369)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbaria, J., Benton, J.; Bimage, K., Blankenburg, K., Bonnin, D.,
Bundy, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, R., Chen, R., Chiu, D., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S.,
Escotto, M., Falls, T., Ewards, C.C., Elhaj, C., Emerling, S.,
Escotto, M., Falls, T., Edwards, C.C., Elhaj, C., Emerling, S.,
Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlak, P.,
Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M.,
Hollows, C., Hollins, B., Homai, F., Howard, S., Huber, J., Hulyk, S.,
Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y.
Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S.,
Lieu, C., Liu, J., Luna, R., Martinez, E., Massey, E.,
Mavhiney, E., McLeod, M.P., Maedor, M., Morries, S., Moser, M.,
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Mguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38491 Trcacaccarratricritrirratrerreraar-rratrirratrirrirratrirratra 38549
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Homo sapiens 12 BAC RP11-359B12 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Pred. No. 4.5e-23;
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vector_side:left"
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16.3%;
Best Local Similarity 86.7%;
Matches 137; Conservative
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B-Raf protein kinase; melanoma; cytostatic; diagnosis; DNA polymorphism; drug screening; chromosome-7q34; gene therapy; BRAF; ds; gene; single nucleotide polymorphism; SNP.
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Listing first 70 summaries
                                                               OM nucleic - nucleic search, using sw model
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comprises the nucleic acid; and determining the presence or absence of an interaction between the test molecule and the nucleic acid or protein. The polymorphic variations are detected at one or more positions in the positions are in linkage disequilibrium with one or more positions in SEQ ID No. 1, or the variation is the haplotype CTTG or ATGA in ADY9428. Detecting the presence or absence of the one or more polymorphic variations comprises hybridizing an oligonuclectide to the nucleic acid sample, where the oligonuclectide hybridizes to a region cadjacent to the polymorphic variation. The proximal polymorphic variation is within a region between about 5 kb 3' of the incident polymorphic variation or variation and about 5 kb 3' of the incident polymorphic variation.

Treating melanoma in a subject alternatively comprises contacting one or more cells of a subject with a duplex RNA nucleic acid. The invention is useful for treating or preventing melanoma. The present sequence is the DNA sequence of the human BRAF gene. 146060 146180 146240 146300 146360 146420 146480 146601 TATGATAATTAGTGAAAACACCCCAAGAATGTTTTATACTTTTAAATTTTTAAAAATTGAAA 146660 ö 180 240 009 099 120 300 360 420 480 540 Sequence 190276 BP; 55599 A; 35097 C; 37143 G; 62425 T; 0 U; 12 Other; TTTTAGTGACAGTTTTAGTCATTTTCCTAATTGAAAGTATCATAAGTAATCCATAAATTT GAAAAAATGTTAACTACTCTGATAAAAAAGTTTTATAGTTTTCCTACTTTTAAGCAAAAT 14301 TCCATAGGGCMTGGTAATTGTAGTTTCAACATTACTTGCAGTTTCAGTTAGTAAATT 146421 TAATTGATTTTACCAAATTTCCATGGAACAAACAAGGTTGGCTATTTTTGGATTGATAT 541 GGAGTTTAGATAGCTAAAGTATAATTTATTTGTGATTTAATAATGGTATGGAGTTAGGC 601 TATGATAATTAGTGAAAACACCCAAGAATGTTTTATACTTTTAAAAATTTTAAAAA ATTAAGCCTAGTAAGTATAATTTAATATTGTCAAATAATTTGGAAAAATACCATGGGTACT TAATTGATTTTACCAAATTTCCATGGAACAAACAAGGTTGGCTATTTTTGGATTGATAT TITGAAATACTAGTACAGGAATATCATTGTTAGTTGAATTTTTAGCCTTAGAAAACAAAT Gaps DB 14; Length 190276; . 0 Indels Match 100.0%; Score 700; DB 14; Local Similarity 99.9%; Pred. No. 5e-110; es 699; Conservative 1; Mismatches 0; 241 181 301 361 421 61 481 Query Match Best Loca Matches 888888888888888888888888 Dp qq g Op ò g Ω g ò ద g Š g à ò ò 8 ò ò ò ò

RESULT 2 AAL05340/c

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Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
                                             Human reproductive system related antigen DNA SEQ ID NO: 8028.
AAL05340 standard; DNA; 19167 BP
                                                                                                                                              2000US-0179065P.
2000US-0180628P.
2000US-0184664P.
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2000US-0189874P.
2000US-0190076P.
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2000US-0227009P.
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2000US-0232398P
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                             21-NOV-2001 (first entry)
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                                                                                                                                             31-JAN-2000;
04-FEB-2000;
02-MAR-2000;
16-MAR-2000;
11-MAR-2000;
11-MAR-2000;
11-MAY-2000;
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11-MAY-2000;
28-JUN-2000;
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14-AUG-2000;
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                                                                                  Homo sapiens
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2000US-0232399P.
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2000US-0233063P.
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2000US-0233063P.
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2000US-023423P.
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                                                                                                                                                    Inolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                               The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; testicular antigen; testes; cancer; metastasis; immune disorder; reproductive system disorder, urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic; gene; ds.
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82.3%; Pred. No. 2.1e-10;
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Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer.
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The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The

Disclosure; SEQ ID NO 2861; 766pp; English

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                                                                                                                                                                                                                                       sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding a protein fragment of the invention
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82.3%; Pred. No. 2.1e-10;
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08-NOV-2000
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08-NOV-2000; 2000US-0246525P.
08-NOV-2000; 2000US-0246526P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246609P.
08-NOV-2000; 2000US-0246611P.
08-NOV-2000; 2000US-0246611P.
17-NOV-2000; 2000US-0249208P.
17-NOV-2000; 2000US-0249208P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249269P.
17-NOV
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2000US-0251869P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JAN-2001;
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Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases. WPI; 2001-541565/60

Rosen CA, Barash SC, Ruben SM

Disclosure; SEQ ID NO 11432; 1701pp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating cc medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. CT the nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and other cancers of the adrenal gland, bone, bone marrow, covarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, crohn's disease, con multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing confectious diseases e.g. cerebral anoxia and epilepsy; and (f) infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 19167 BP; 5592 A; 3875 C; 3876 G; 5824 T; 0 U; 0 Other;

38-NOV-2000;

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The present invention describes genes containing coding mononucleotide repeats (cMMRs). The genes are useful for the development of an antibody against MSI-H (hugh microsatellite instability) tumour. Also described:

(1) cDNA genes containing cMMRs with 10 or more nucleotide sequences, and selected from the cDNA genes having the nucleotide sequences of SEQ ID (NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41 and 43; (2) cDNA genes, which are frameshift mutated DNA deletion or insertion of one or more base in the cMNRs; (3) genomic DNA deletion or insertion of one or more base in the cMNRs; (3) genomic DNA genes containing cMNRs with 10 or more nucleotide sequences, and selected from the genomic DNA genes having the nucleotide sequences of SEQ ID (SEC) 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42 and 44; and (4) genomic DNA genes, which are frameshift mutated by deletion or insertion of one or more base in the cMNRs. The genes have cytostatic activity. The present sequence represents an MSI-H carcinoma genomic DNA sequence from the present invention.
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                                                                                                9059 Traraacraacritriririririririsegecriggaaarcrirrrrrrrraarrraarrirarr 9118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genes containing coding mononucleotide repeats are useful in developing an antibody against MSI-H (hugh (sic high) microsatellite instability)
                                                                4 TITCACATAAAGITITITITITITITAATAAAAAAAATATTITITAATA
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        coding mononucleotide repeat; cMNR; gene; antibody; MSI-H tumour; MSI-H carcinoma; high microsatellite instability tumour; high microsatellite instability carcinoma; cytostatic; ds.
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0
Length 19167;
                                  Indels
                                                                                                                                                                                                                                 9179 Atacatérecearerregrecrececerrale 9216
                                                                                                                                                                                                   ATACATGTGCCATGCTGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                         MSI-H carcinoma genomic DNA sequence SEQ ID NO:34.
DB 5;
                                  28;
Score 113.2; DB 5
Pred. No. 2.1e-10;
                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhee HS;
                                                                                                                                                                                                                                                                                                                 ADQ59197 standard; DNA; 155225
16.2%;
82.3%;
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                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                               Conservative
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               Similarity
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KIM N G.
LEE J S.
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               Best Local Simi
Matches 130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JAN-2004
                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                      ADQ59197;
 Query Match
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(LEEJ/)
(RHEE/)
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Multiple myeloma; secreted; cancer; haematopoietic disease; anaemia;

Multiple myeloma; reproductive system disorder; prostatitis;

Multiple myeloma; reproductive system disorder; prostatitis;

Multiple myeloma; musculoskeletal disease; systemic lupus erythematosus;

Whyernatraemia; fetal disease; arrhythmia; hypernatraemia; fetal disease;

Wetal alcohol syndrome; Down's syndrome; excretory disease;

Whyernaty incontinence; renal disorder; neural; sensory disease;

Murinary incontinence; renal disorder; neural; sensory disease;

Multiple bowel syndrome; epithelial disease; diabetes;

Multiple bowel syndrome; epithelial disease; soleroderma;

Multiple bowel syndrome; epithelial disease; soleroderma;

Multiple powel syndrome; epithelial disease; antiathritic;

Multiple myenietic; anti-HIV; immunosuppressive; antianflammatory;

Multiple myenietic; antibacterial; osteopathic; dermatological; antigout;

Multiple myenic; uropathic; neuropicotective; antiparkinsonian; tranquilizer;

Multidiabetic; anabolic; hypertensive; vulnerary; ds.
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                                                                                                                                                                                                                                                                                                                                                                      DNA fragment of a BAC clone that encodes a human secreted protein Seq354.
                                                                               Sequence 155225 BP; 44334 A; 29321 C; 30431 G; 51139 T; 0 U; 0 Other;
                                                      Gaps
                           Length 155225
                                                      ö
                                                   28; Indels
                                                                                                                                                                                                                  138580 ATACATGTGCCATGTGGTGTGCTGCACCCATTAACTC 138617
                                                                                                                                                                                       ATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
                         Score 113.2; DB 12;
Pred. No. 2e-10;
                                                    0; Mismatches
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97US-0061527P.
97US-0061528P.
97US-0061536P.
97US-0071498P.
98WO-US021142.
99WG-US021142.
                         16.2%;
                                                                                                                                                                                                                                                                                     ADJ12500 standard; DNA; 8766
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                                                    Matches 130; Conservative
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FLORENCE K A
GREENE J M.
YOUNG P E.
FERRIE A M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BREWER L A.
DUAN R D.
                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROSEN C A.
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09-OCT-1997;
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                                                                                                                                                                                                                                                                                                                ADJ12500;
                         Query Match
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(GREE/)
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(RUBE/)
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(Xngg/)

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This invention relates to novel polynuclectides encoding human secreted proteins. Specifically, it refers to the vectors, host cells, recombinant and synthetic methods for producing human polynucleotides, polypeptides can antibodies. Furthermore, it relates to screening methods to identify agonists and antagonists that can be used to inhibit or enhance the production and function of the secreted proteins. The present invention chescribes these compositions as cancer, haematopoietic diseases including preventing disorders such as cancer, haematopoietic diseases including prostatitis and multiple myeloma, reproductive system disorders including prostatitis and inguinal hernia, musculoskeletal diseases including prostatitis and hypernatraemia, mixed fetal diseases including carrinary incontinence and renal disorders, neural of seases including allochol syndrome and bown's syndrome, excretory diseases including curinary incontinence and renal disorders, neural or sensory disease including diabetes and occupational lung disease, endocrine diseases including portal hypertension and irritable bowel syndrome and connective tissue or cipithelial diseases including scleroderma and connective tissue or cuttion through an activites such as cytostatic, antianemic, antidiabetic, antianemic, antidiabetic, antianemic, antidiabetic, antidiabetic, antidiabetic, antidiabetic, antidiabetic, antidiabetic, antidiabetic, antidiabetic antidiabetic, antidiabetic, antidiabetic, antidiabetic, antidiabetic antidiabetic antidiation of the invention, where the printed specification but has been obtained in the printed specificat
                                                                                                                                                                                                                             New isolated nucleic acids and polypeptides, useful for diagnosing, treating, preventing or ameliorating diseases or disorders e.g. cancer, anemia, arthritis, asthma, inflammatory bowel disease or Alzheimer's
                                                                                                          Greene JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8766 BP; 2308 A; 1479 C; 1597 G; 3382 T; 0 U; 0 Other;
                                                                                                                                  Olsen H;
                                                                                                       Florence KA,
                                                                                                                                  Ebner R,
                                                                                                       D, Ruben SM,
Florence C,
                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 354; 286pp; English.
                                                                                                          Duan RD,
                                                                                                                                  Yu G,
                                                                                                          Brewer LA,
Ferrie AM,
                                                                                                                                                                               WPI; 2004-090518/09
(FLOR/) FLORENCE C.
(EBNE/) EBNER R.
                       EBNER R.
OLSEN H.
                                                                                                       Rosen CA,
Young PE,
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                                                                               44 TATCATTTTCTTTTTTATTATTATTATACTTTTAAGTTTTTAGGGTACATGTGCAAAGTG 103
                                                                                                                   61
                                                                                                                                                       104 TGCAGGTTAGTTACATATATATACATGTGCCAGGGTGGTGCTGCACCCATTAACTC 161
                                                                                                                                                                           TTTTATTTTTATTTTTTTTATTATTATTATACTTTTTAAGTTTTTAGGGTACATGTGCACAATG
                                         0; Gaps
   DB 12; Length 8766;
Query Match
Best Local Similarity 94.1%; Pred. No. 2.6e-09;
Matches 111; Conservative 0; Mismatches 7; Indels
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Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer;
                                                                           Tumour suppressor gene derived chemically modified sequence #27
                                                    (first entry)
                                                  18-DEC-2001
XXEX DX XXX
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ВР

AAS46305 standard; DNA; 8666

RESULT 7 AAS46305 AAS46305;

The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes bisulphite, of genes associated with tumour suppression and oncogenes by a sequence taken from 536 (actually 533 since numbers 408, 458 and sequence 500 are missing from the sequence listing) sequences (Ss) and sequences compared to the complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleide polymorphisms and also to be used in an array for analysing classacs and so be used in a method for ascertaining genetic and/or proposed in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the 513 genomic sequences derived from tumour suppressor genes and oncogenes. Note: The sequence deate for this parent did not form part of the printed specification, but we will appear to the present of the printed specification, but and the compared of the pr 1667 GTTATGTTGGTGTTGTATTTATTTA-TTATTTAGTATTAGGTATATTTTAAT 1725 1726 GİTATITITITITITITITITITI 1785 AİTTA TARA GALI 1785 Fragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. cancer. 132 GCCATGCTGGTGCTGCACCCATTAACTCACATGAAGTTTTTTAAATTTTAGTGACA 191 1607 TATTTTAAGTTTTAGAGTATATGTGTATAATGTGTAGGTTTGTTATATGTATATGT 72 ACTITITAAGITITIAGGGTACAIGIGCAAAGIGIGCAGGITAGITACATATATATACAIGT GTTTTAGTCATTTTCCTAATTGAAAGTATCATAAGTAATCCATAAATTTTGAAAAAAATGT Gaps ä Sequence 8666 BP; 2444 A; 168 C; 1868 G; 4186 T; 0 U; 0 Other; Length 8666; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP; 0; Mismatches 324; Indels Score 106.6; DB 4; Pred. No. 2.9e-09; ftp.wipo.int/pub/published\_pct\_sequences Claim 1; SEQ ID NO 27; 27pp; English Berlin K; 15-MAR-2000; 2000DE-01013847. 06-APR-2000; 2000DE-01019058. 07-APR-2000; 2000DE-01019173. 30-JUN-2000; 2000DE-01043826. 01-SEP-2000; 2000DE-01043826. 15.2%; .5-MAR-2001; 2001WO-EP002955. Best Local Similarity 49.0 Matches 312; Conservative cytosine methylation; ds Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2001-602752/68 Local Similarity WO200168912-A2 Homo sapiens 20-SEP-2001 192 Query Match Olek A, g g ò 쉽 ò ò

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2025
                             2026 TTTAGAGAAATTTTGAATTTATTGAAAGTTTTATTTAGAAATATATGTGTAAGTGAATA 2085
                                                                                                                                                                                                                                                                                                                                  431
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                                                                                                                                                                                                                                                                                                         611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences
252 TAACTACTCGATAAAAAGTTTTATAGTTTCCTACTTTTAAGCAAAATTCCATAGGGCA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiarteriosclerotic, antianaemic, cytostatic, nootropic, neuroprotective, anti-HIV; anticonvulsant; ophthalmological, antirhematic, antiarthitic; antidiabetic, antipsoriatic, antiinflammatory, cancer; eye disease, arteriosclerosis, anaemia, acute myeloid leukaemia, Alzheimer's disease, AIDS; epilepsy; neurofibromatosis, rheumatoid arthritis; psoriasis; bowel disease; gene,
                                                                                                                                                                                                             1966 GTTATATATATATATAAGAGTTGAAAGAGTTTTTGGATGTAGGAATTTATGGTAGGT
                                                                                                                                                                                                                                          492 AGTACAGGAATATCATTGTTAGTTGAATTTTTAGCCTTAGAAAACAAATGGAGTTTAGAT
                                                                                                                       TAAGTATAATTTAATATTGTCAAATAATTTGGAAAATACCATGGGTACTTAATTGATTTT
                                                                                                                                                                                432 ACCAAATTTCCATGGAACAAAGATGGTTGGCTATTTTTTGGATTGATATTTTTGAAATACT
                                                           312 TGGTAATTGTAGTTTCAACATTACTTGCAGTTTCAGTTAGTAAATATTAAGCCTAG
                                                                                                                                                                                                                                                                                                      552 AGCTAAAGTATATTTTGTGATTTAATAATGGTATGGAGTTAGGGCTATGATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid comprising fragment of chemically modified gene, useful diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 369; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                               2146 ATAGATTTTTGAAGGAGTTTATTTTTTTTTTTTTTT 2182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immune system associated gene SEQ ID NO: 369.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 TAACTACTCTGATAAAAAGTTTTATAGTTTTCCTACTTTTAAGCAAAATTCCATAGGGCA 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAGTATAATTTTAATATTGTCAAATAATTTGGAAAATACCATGGGTACTTAATTGATTTT 431
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                                      acute myeloid
can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                            ACTITITAAGTITITAGGGTACATGTGCAAAGTGTGCAGGTTAGTTACATATATACATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTTTAGTCATTTTCCTAATTGAAAGTATCATAAGTAATCCATAAATTTTGAAAAAAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  432 ACCAAATTTCCATGGAACAAACAAGGTTGGCTATTTTTTGGATTGATATTTTGAAATACT
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                                                                                                                                                                                                           Gaps
                                                                                                                                                                     15.2%; Score 106.6; DB 6; Length 8666;
49.0%; Pred. No. 2.9e-09;
                                                                                                                                  Sequence 8666 BP; 2444 A; 168 C; 1868 G; 4186 T; 0 U; 0 Other;
                                                                                                                                                                                    Pred. No. 2.9e-09;
0; Mismatches 324; Indels
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                                                                                                                                                                                    Local Similarity 49.0
nes 312; Conservative
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The invention relates to a nucleic acid comprising a sequence (I) of at least 18 bases in length of a segment of chemically pre-treated genomic DNA which has any one of the sequences of (ABR33919-ABR3403) or its complement. Also included are an oilgonuclectide or peptide nucleic acid (I), probes for detecting cytosine methylation or single-complement for (I), probes for detecting cytosine methylation or single-conclected polymorphisms (SNP) in (I), an array of oligomers or peptide nucleic acids for analyging diseases associated with the methylation craft ferentiation, analyging diseases associated with the methylation craft are analyging diseases associated with the methylation craft and/or epigenetic parameters, classification, differentiation, grading staging, treatment and/or diagnosis of attrocytomas, or the predisposition to astrocytomas by analysing cytosine methylations, involves obtaining a biological sample containing genomic or morethylated at the 5-position, in the genomic DNA sample, to uracil or annother base which is dissimilar to cytosine in terms of hybridisation contained behaviour. by chemical treatment and amplifying chemically pre-treated genomic DNA fragments using the array and a polymerase, where the amplificates carry a detectable label. The method further involves containing a methylation status of one or more cytosine positions, and contained are the genomic DNA is chemically treated by using a containing an experience to one or more data sets. The genomic DNA is chemically treated by using a fluctorescent label or radionuclide. Optionally, the labels of the cytosine position are single positions or missue, based on the specific genomic methylation attaus of brain cities are detectable molecule fragments having a typical mass spectrometer. The fragments of chemically contained by the amplificates are detected in a mass spectrometer. The fragments of chemically certered genomic DNA to be amplified, have a single position many detected by matrix assisted laser descorption mass spectromet
                                                                                                                                                                                                                                                                                                                                                        Novel chemically modified genomic DNA sequences, useful in the characterization, classification, differentiation, grading, staging, treatment and/or diagnosis of astrocytomas or predisposition to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 95; 37pp; English
                                                                                                                                                                                                                                                                       Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification,
                                                                                                            02-JUL-2001; 2001WO-EP007538.
                                                                                                                                                         30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                       Piepenbrock C,
                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention. Note:
the printed specif
                                                                                                                                                                                                                                                                                                                  WPI; 2002-171649/22
                  WO200202808-A2
                                                               10-JAN-2002
                                                                                                                                                                                                                                                                       Olek A,
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form part
(MALDI) or using electron spray mass spectrometry (ESI). The present sequence is one of the chemically pre-treated reference DNA samples of the invention. Note: The sequence data for this patent did not form par
                                                                                                                                                                                               directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                   Sequence 8666 BP; 2444 A; 168 C; 1868 G; 4186 T; 0 U; 0 Other;
                                                                                                                                                   in electronic
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                                            1; Gaps
                     0; Mismatches 324; Indels
  DB 6;
15.2%; Score 106.6; DB 649.0%; Pred. No. 2.9e-09;
                      Conservative
 Query Match
Best Local Similarity
Matches 312; Conserv
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New nucleic acid fragments from chemically treated angiogenesis-

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1726 GTTATTTTTTTTTTTTTTTTTATAGATTTATAAGATTTATAATGGATAATGGATTTTAATTTT 1785
                                                                                                                                                                                              2026 TTTPAGAGAAATTTTTGAATTTTTGAAAGTTTTATTTAGAAATATATGTGTAAGTGAATA 2085
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                                               Human; angiogenesis; methylation; eye disease; glaucoma; tumour;
inflammation; rheumatorid arthritis; disbetic retinopathy; antiulcerds;
macular degeneration; inflammatory bowel disease; Crohn's disease;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
GTTATGTTGGTGTGTTTTATTTATTTA-TTATTTAGTATTAGGTATATTTAAT
                                                                                                                                                                   252 TAACTACTCTGATAAAAAAGTTTTATAGTTTCCTACTTTTAAGCAAAATTCCATAGGGCA
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                                                                                                          GTTTTAGTCATTTTCCTAATTGAAAGTATCATAAGTAATCCATAAATTTGAAAAAAATGT
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US-09-949-016-77443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15524, A Sequence 15524, A Sequence 15344, A Sequence 13348, A Sequence 2044, Ap Sequence 448, App Sequence 13173, A Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309, App Sequence 309
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Sequence 469, App
Sequence 134975,
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Sequence 14000, A
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Sequence 15754, A
Sequence 15970, A
Sequence 15091, A
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6821.751 Million cell updates/sec
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'EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

'EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*

'EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*

'EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

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1 ctgtttcacataaagtttt.....gccttttaggtgatgtggca
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               GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-949-016-13358

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US-09-949-002-1033

US-09-949-016-13564

US-09-949-016-13674

US-09-949-016-15654

US-09-949-016-12654

US-09-949-016-12654

US-09-949-016-12654

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                                                                                                                                                                                                                                                                                                                                      1403666 seqs, 935554401 residues
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14.9 601
14.9 256171
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14.8 86980
14.7 601
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Perfect score:
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426, App
454, App
15703, A
16066, A
150430,
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32, Appl
138, Appl
13828, A
1542, Ap
11830, A
11830, A
1182, A
11930, A
11930, A
11911, A
11911, A
11911, A
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12611, A
14413, A
15473, A
13404, A
16065, A
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342, App
15744, A
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16061, A
13027, A
14577, A
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59510, A
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16065, A
13675, A
12386, A
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US-09-984-429-426
US-09-984-429-454
US-09-949-016-154030
US-09-949-016-154030
US-09-949-016-134040
US-09-949-016-134040
US-09-949-016-13413
US-09-949-016-13413
US-09-949-016-13413
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US-09-949-016-13675
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## T T CHIMIDIAN

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RESULT 197443

Sequence 77443, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASEEQ for Windows Version 4.0

SEQ ID NO 77443

LENGTH: 601
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ORGANISM: Homo sapiens
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US-09-984-429-469/C
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Sequence 14000 Application US/09949016

Fatent No. 681239

FATENT NO. 681239

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-0-0-03

PRIOR FILING DATE: 2000-0-0-03

PRIOR PILING DATE: 2000-0-0-03

NUMBER OF SEQ ID NOS: 207012

SOCTWARE: FREESEQ for Windows Version 4.0
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84.6%; Pred. No. 4.9e-13;
tive 0; Mismatches 23;
                                                                        16.0%; Score 112.2; DB 3;
1larity 84.6%; Pred. No. 3.9e-13;
Conservative 0; Mismatches 23;
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US-09-984-429-354
i Sequence 354, Application US/09984429
j Patent No. 7026447
j GENERAL INFORMATION:
j APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (1)...(154626)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 84.6
Matches 126; Conservative
                                                                                          Best Local Similarity
Matches 126; Conserv
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                    ; ORGANISM: Human
US-09-949-016-77443
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LENGTH: 154626
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TYPE: DNA
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44 TATCATTTTTTTTTTATTATTATTATACTTTTAAGTTTTAGGGTACATGTGCAAAGTG 103
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Pred. No. 4.8e-12;
0; Mismatches 7;
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Fatent No. 702647
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: PZ018P2
CURRENT FILING DATE: 2001-10-30
PRIOR PILING DATE: 2000-11-01
PRIOR PLING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR PLING DATE: 1997-10-09
PRIOR PLING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR PLING DATE: 1997-10-09
FILE REFRENCE: PZ018P2
CURRENT APPLICATION NUMBER: US/09/984,429
CURRENT APPLICATION NUMBER: US/09/984,429
CURRENT FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1997-00-08
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
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PRIOR PRILING DATE: 1997-10-09
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PRIOR PLILING DATE: 1997-10-09
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Best Local Similarity 94.1%;
Matches 111; Conservative
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TYPE: DNA
ORGANISM: Human
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ORGANISM: Human
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Fatent No. 6812339
GENERAL INFORMATION
GENERAL INFORMATION:
TITLE OF INVENTION: DOLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
FRIOR PPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                       18893 TAAGTITITAGGGTACATGTGCACATTGTGCAGGTTAGTTACATATGTATACATGTGCCAT 18834
                                                                                                                                                                                                                                                                           290 TIATATACTIGTTTGCCATCTGTATAATTTCTTTATTTTTTTTTATTATTATATATTT 231
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                                                                                                                                                                             Length 42595;
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                                                                                                                                                                           DB 5;
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82.6%; Pred. No. 1.5e-11;
iive 0; Mismatches 25;
                                                                                                                                                                          Score 104.2; DB 5
Pred. No. 1.6e-11;
0; Mismatches 18
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                                                                                NAME/KEY: misc feature

: LOCATION: (7234)..(7234)

: OTHER INFORMATION: n equals a,t,g, or c

US-09-984-429-469
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; Patent No. 6812339
                                                                                                                                                                          Query Match
Best Local Similarity 86.9%;
Matches 126; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 82.6
Matches 119; Conservative
              LENGTH: 42595
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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SEQ ID NO 469
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLOO1307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 12822

LENGTH: 2556171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPRICANT: VENTER, J. Craig et al.
APPRICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PELING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTESEQ for Windows Version 4.0
SEQ ID NO 15524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89341 AAGTTTTAGGGTACATGTGCACAATGTGCAGGTTAGTTACATATGTATACATGTCCATG 89400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 256171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 14.9%; Score 104; DB 3; Length 25
Best Local Similarity 82.6%; Pred. No. 1.9e-11;
Matches 119; Conservative 0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89401 CTGGTGTGCTGCACCCATTAACTC 89424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 CTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 15524, Application US/09949016; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                             | FEATURE:
| NAME/KEY: misc_feature
| LOCATION: (1)...(256171)
| OTHER INFORMATION: n = A,T,C or G
| US-09-949-016-12822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)...(256176); OTHER INFORMATION: n = A,T,C or GUS-09-949-016-15524
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82.6%;
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NAME/KEY: misc_feature
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Best Local Similarity
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Patent No. 6900016
GENERAL INFORMATION:
Requence 2044 Application US/09949002
Fatent No. 6900016
GENERAL INFORMATION:
RAPPLICANT: VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENTEX, VENT
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| Patent No. 6900016
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 TAAGTTTTAGGGTACATGTGCACATGTGCAGGTTAGTTACATATGTACATGTGCCAT 142
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                                                                                                                                                                                                                                                            Length 260247;
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86.2%; Pred. No. 2.7e-11;
tive 0; Mismatches 19;
                                                                                                                                                                                                                                                               Score 102.8; DB 3;
Pred. No. 3.3e-11;
0; Mismatches 27;
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13358
LENGTH: 260247
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                                                                                                                                                                                                                                                                  14.7%;
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Best Local Similarity 82.33
Matches 130; Conservative
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Best Local Similarity 86.2
Matches 125; Conservative
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US-09-949-002-2044/c
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                                                                                                                                                   TYPE: DNA
ORGANISM: Human
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FACURE NO. SEL2ASI

FACURE NO. SEL2ASI

FACURE NO. SELZASI

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFRENCE: CLOOL307

CURRENT FILING DATE: 2000-04-14

FRIOR APPLICATION NUMBER: 60/241,755

FRIOR APPLICATION NUMBER: 60/241,768

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFFWARE: FREUESEQ for Windows Version 4.0

LENGTH: 86980
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Bacent No. 6812339

GENERAL INFORMATION:
APPLICAMY: VENTER, J. Craig et al.
TITLE OF INVENTION:
TITLE OF INVENTION:
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03
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      Indels
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Pred. No. 2e-11;
0; Mismatches 27;
                                                                18 TITITITITIGATGATTTTTAATAAATATCATTTTCTTT
      0; Mismatches
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US-09-949-016-15344/c
; Sequence 15344 Application US/09949016
; Patent No. 6812339
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Best Local Similarity 81.6%;
Matches 120; Conservative
      Matches 119; Conservative
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Sequence 622, Application US/09949002
| Sequence 622, Application US/09949002
| Patent No. 6900016
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: MITH INFLAMMATORY AUTOIMMUE DISEASE, METHODS OF DETECTION
| TITLE OF INVENTION: AND USES THEREOF
| FILE REFERENCE: CL000790
| CURRENT APPLICATION NUMBER: US/09/949,002
| CURRENT FILING DATE: 2000-01-28
| PRIOR PAPLICATION NUMBER: 60/231,401
| PRIOR PAPLICATION OF SEQ ID NOS: 10823
| SOFTWARE: FascSEQ for Windows Version 4.0
| SEQ ID NO 622
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86.2%; Pred. No. 3.2e-11;
live 0; Mismatches 19;
                PRECENT NO. 7026447.

PRECENT NO. 7026447.

APPLICANT: Rosen et al.

ITLE OF INVENTION: 53 Human Secreted Proteins
FILTE OF INVENTION: 53 Human Secreted Proteins
FILE OF INVENTION: 8201822.

CURRENT APPLICATION NUMBER: US/09/984,429

CURRENT FILING DATE: 2000-11-01

PRIOR FILING DATE: 2000-11-01

PRIOR FILING DATE: 1999-04-08

PRIOR APPLICATION NUMBER: PCT/US98/21142

PRIOR PILING DATE: 1999-04-08

PRIOR APPLICATION NUMBER: 60/061,463

PRIOR PILING DATE: 1997-10-09

PRIOR PILING DATE: 1997-10-09

PRIOR PILING DATE: 1997-10-09

PRIOR APPLICATION NUMBER: 60/061,529

PRIOR PILING DATE: 1997-10-09

PRIOR APPLICATION NUMBER: 60/061,536

PRIOR PILING DATE: 1997-10-09

PRIOR SPELICATION NUMBER: 60/061,536

PRIOR PILING DATE: 1997-10-09

PRIOR PELING DATE: 1997-10-09

PRIOR PILING DATE: 1997-10-09
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Matches 125, Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Human
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Patent No. 6900016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THERBOF
TITLE OF INVENTION: AND USES THERBOF
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                           14.7%; Score 102.6; DB 3; Length 601; 86.2%; Pred. No. 2.7e-11; ive 0; Mismatches 19; Indels 1
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86.2%; Pred. No. 3.2e-11;
vative 0; Mismatches 19;
                     FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
FRIOR APPLICATION NUMBER: 60/231,401
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 2045
LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            440 GCTGGTGTGCTGCACCCATTAACTC 416
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     AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 125; Conservative
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Best Local Similarity
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                , ORGANISM: Human
US-09-949-002-2045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
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US-09-984-429-448/c
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                                                                                                                                                                                                                                                              TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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1; Gaps

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; ORGANISM: Homo sapiens
US-09-984-429-309
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                 AREDICANT: UNEXPER, J. Craig et al.
APPLICANT: UNEXPER, J. Craig et al.
APPLICANT: UNEXPER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRASESEQ FOR WINDOWS Version 4.0
SEQ ID NO 13173
LENGTH: 360470
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                                                              17 TITITITITITGALGALTITLAATAAAATAICAITITICITITITITITATTATAACTIT
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                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
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                         Indels
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86.2%; Pred. No. 3.6e-11;
iive 0; Mismatches 19;
    Pred. No. 3.2e-11;
0; Mismatches 19;
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| Sequence 309, Application US/09984429
| Patent No. 7026447
| GENERAL INPORMATION:
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: 53 Human Secreted Proteins
| TITLE OF INVENTION: 53 Human Secreted Proteins
| FILE REPERENCE: PZ018P2
| CURRENT APPLICATION NUMBER: US/09/984,429
| CURRENT FILING DATE: 2000-11-01
| PRIOR FILING DATE: 2000-11-01
| PRIOR FILING INTE: 1999-04-08
| PRIOR APPLICATION NUMBER: 09/288,143
| PRIOR APPLICATION NUMBER: PCT/US98/21142
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                                                                                                                                                                                                                          137 GCTGGTGTGCTGCACCCATTAACTC 161
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86.2%;
    Best Local Similarity 86.2
Matches 125, Conservative
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Matches 125; Conservative
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Pred. No. 3.8e-11;
0; Mismatches 41; Indels 2;
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Pred. No. 3.5e-11;
0; Mismatches 6;
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/061,463
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,527
PRIOR APPLICATION NUMBER: 60/061,537
PRIOR PILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
SPRIOR FILING DATE: 1997-10-09
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; LCCATION: (1)...(194889)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-15654
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Best Local Similarity 77.6%;
Matches 149; Conservative
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Best Local Similarity 94.6%;
Matches 106; Conservative
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FACENTEAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOO1307
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 15367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FERUELL NO. 101423)

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT FILING DATE: 2000-04-14

CURRENT FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR PELICATION NUMBER: 60/231,768

PRIOR PELICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOCTWARE: FastSEQ for Windows Version 4.0

LENGTH: 353032
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                                                                                                                                                                  Sequence 15367, Application US/09949016
Patent No. 6812339
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; Sequence 12415, Application US/09949016
; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 81.6
Matches 129; Conservative
                                                                 206 CATTAACTC 214
                          153 CATTAACTC 161
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15367
                                                                                                                               RESULT 19
US-09-949-016-15367
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ORGANISM: Human
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107969 TAC-TITAAGTITTTAGGGTACATGTGCACATTGTGCAGGTTAGTTACATATGTATACATG 108027
                                                                                 TGCCATGCTGCTGCTGCACCCATTAACTC-ACATGAAGTTTTTTTAAATTTTAGTGA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 TGTGCAAAGTGTGCAGGTTAGTTACATATATATGTGCCCATGCTGGTGTGCTGCACC 152
                                                                                                                                                                                                                                                                                                            APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US. REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR PILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Parent.pm
SSC ID NO 18942
LENGTH: 325
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                                                                                                                                                                                                                                                                    . Sequence 18942, Application US/09513999C ; Patent No. 6783961
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Best Local Similarity 83.71
Matches 108; Conservative
                                                                                                                          190 CAGTTTTAGTCA 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 124.
OTHER INFORMATION: w=a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 130
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US-09-513-999C-18942
                                           131
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TYPE: DNA
ORGANISM: Human
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                              US-09-949-016-15970
                                                                                                                                                                                                                                                                                 LENGTH: 181251
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASESEQ FOR WINDOWS VERSION 4.0

SEQ ID NO 15754
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Best Local Similarity 79.9%; Pred. No. 7.3e-11;
Matches 119; Conservative 0; Mismatches 30; Indels 0;
                                                                               Length 363032;
                                                                             Query Match 14.4%; Score 101; DB 3; Length 36 Best Local Similarity 79.9%; Pred. No. 7.3e-11; Matches 119; Conservative 0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                76721 CATGCTGGTGCGCTGCACCCACTAACTCA 76749
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Sequence 15970, Application US/09949016
Parent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-949-016-15754
; Sequence 15754, Application US/09949016
; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(363033)
COTHER INFORMATION: n = A,T,C or G
; LOCATION: (1)...(363032)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12415
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RESULT 23
US-09-949-016-15091/c
i Sequence 15091, Application US/09949016
j Patent No. 6812339
i GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
PILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
pRIOR APPLICATION NUMBER: 60/241,755
pRIOR APPLICATION NUMBER: 60/241,755
pRIOR PELING DATE: 2000-10-20
pRIOR PELING DATE: 2000-10-03
pRIOR FILING DATE: 2000-10-03
pRIOR FILING DATE: 2000-10-03
pRIOR FILING DATE: 2000-09-08
pRIOR FILING DATE: 2000-09-08
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

NUMBER: FASTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 TAGTCATTTTCCTAATTGAAAGTATCATAAGTAATCCATAAATTTTGAAAAAAATGTTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 100.8; DB 3 Pred. No. 7.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15091
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Best Local Similarity 64.5%;
Matches 182; Conservative
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Sequence 15703, Application US/09949016
; Sequence 15703, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VEYTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    TURENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15703
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Pred. No. 7.5e-11;
0; Mismatches 21;
                                                                    APPLICANT: Rosen et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: PZ018P2
                                                                                                                                           FILE REFERENCE: PZO18P2
CURRENT APPLICATION NUMBER: US/09/984,429
CURRENT FILING DATE: 2001-10-30
PRIOR PELICATION NUMBER: 60/244,591
PRIOR PELICATION NUMBER: 09/288,143
PRIOR PELICATION NUMBER: 09/288,143
PRIOR PILING DATE: 1999-04-08
PRIOR PILING DATE: 1999-04-08
PRIOR PILING DATE: 1999-10-08
PRIOR PILING DATE: 1997-10-09
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Best Local Similarity 84.9%;
Matches 124; Conservative (
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                               79 AGTITITAGGGIACAIGTGCAAAGTGTGCAGGTTAGTTACATATATATACATGTGCCATGC 138
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                                                                       0; Gaps
Score 100.8; DB 3; Length 193169;
Pred. No. 7.8e-11;
0; Mismatches 27; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 426, Application US/09984429
Patent No. 7026447
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: PZ018P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE KEREAKMER: FALIBER

CURRENT PILING DATE: 2001-10-30

PRIOR PILING DATE: 2001-10-30

PRIOR FILING DATE: 2001-11-01

PRIOR FILING DATE: 2000-11-01

PRIOR FILING DATE: 1999-04-08

PRIOR FILING DATE: 1999-04-08

PRIOR PILING DATE: 1999-06-06

PRIOR PILING DATE: 1999-06-06

PRIOR PILING DATE: 1999-10-09

PRIOR PILING DATE: 1997-10-09

PRIOR FILING DATE: 1997-10-09

NUMBER OF SEQ ID NOS: 727

SCOTWARE: PATENT VOET: 2.0

SEQ ID NO 426

LENGTH: 1055
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US-09-984-429-454/c
; Sequence 454, Application US/09984429
14.4%;
81.2%;
                                  Best Local Similarity 81.2
Matches 117; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-984-429-426/c
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                                                                                                                                                                                                                                                                                                                                                                                              139
   Query Match
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TYPE: DNA ORGANISM: Human

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Gaps 1,

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FILE REFERENCE: CL001307
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ORGANISM: Human
                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
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Fatent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR FILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FESESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-949-016-150430

Sequence 150430, Application US/09949016
Patent No. 681239
GENERAL INFORMATION:
A PAPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                                                                                  1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
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14.3%; Score 100.4; DB 3; Length 144362;
Best Local Similarity 82.5%; Pred. No. 9.2e-11;
Matches 127; Conservative 0; Mismatches 26; Indels 1;
                                  Length 91538;
                                                                               Indels
                                    Query Match 14.3%; Score 100.4; DB 3; Best Local Similarity 84.9%; Pred. No. 9e-11; Matches 124; Conservative 0; Mismatches 21;
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                                                                                                                                                                                                                                                                                                                136 TGCTGGTGTGCTGCACCCATTAACTC 161
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NAME/KEY: misc_feature
LOCATION: (1)...(144362)
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-949-016-16066
US-09-949-016-15703
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LENGTH: 144362
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

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Best Local Similarity 81.5%; Pred. No. 9.6e-11;
Matches 128; Conservative 0; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     14.3%; Score 100.2; DB 3; 71.2%; Pred. No. 8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 08/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 150430
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 13420
LENGTH: 47363
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Patent No. 6812339
GENERAL INFORMATION:
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OTHER INFORMATION: n = A,T,C or G
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Matches 146; Conservative
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NAME/KEY: misc_feature
LOCATION: (1)...(135476)
CTHER INFORMATION: n = A,T,C or G
US-09-949-016-14413
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COTHER INFORMATION: n = A, T, C or G
US-09-949-016-15473
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86.0%;
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Best Local Similarity 89.3%;
Matches 108; Conservative
    PRIOR FILING DATE: 2000-09-08
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Best Local Similarity
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ORGANISM: Human
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Sequence 12611, Application US/09949016

Patent No. 681239

FAPELICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYNORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR PELICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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Facent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
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41 AAATATCATTTTCTTTTTTTTTTTTTTTTTTTAGGTTTTTAGGGTACATGTGCAAA 100
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Pred. No. 1e-10;
0; Mismatches 13; Indels 0;
                                                                                                                                                   TACATGTGCCATGCTGGTGCTGCACCCATTAACTC 161
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12611
LENGTH: 135476
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12611
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Best Local Similarity 89.3%;
Matches 108; Conservative (
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gequence 15473, Application US/09949016

patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WINDER: US/09/949,016

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103306 ATGTGCAGGTTAGTTACATATGTATACATGTGCCATGCTGGTGTGTGCTGCACCCACTAACT 103247
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Pred. No. 1e-10;
0; Mismatches 13; Indels 0;
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Pred. No. 1.1e-10;
0; Mismatches 18;
NUMBER OF SEQ ID NOS: 207012
SOFTWARER: FastSEQ for Windows Version 4.0
SEQ ID NO 14413
LENGTH: 135476
TYPE: DNA
ORGANISM: Human
FEATURE:
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18 TITITITITIGATGATTTTAATAAATATCATTT
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Best Local Similarity 80.1%;
Matches 117; Conservative
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US-09-245-041-16
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFREENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,768
PRIOR FILING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTHARE: PASESEC for Windows Version 4.0
SEQ ID NO 16065
                                                                                                                                GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-0414
PRIOR PILING DATE: 2000-04-02
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 13404
LENGTH: 237863
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Pred. No. 1.2e-10;
0; Mismatches 27; Indels 0;
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Best Local Similarity 80.6%; Pred. No. 1.1e-10;
Matches 129; Conservative 0; Mismatches 30; Indels 1;
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                                                                                          ; Sequence 13404, Application US/09949016; Patent No. 6812339
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Patent No. 6812339
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81.1%;
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Best Local Similarity 81.1
Matches 116; Conservative
321248 CATTAACTC 321256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Human
US-09-949-016-16065
                                                                             US-09-949-016-13404
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Sequence 16, Application US/09245041
; Betent No. 6274339
; Genverce 16, Application US/09245041
; Patent No. 6274339
; GENVERAL INFORMATION:
; APPLICANT: Nagle, D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
; TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY
; FILE REFERENCE: 7853-136
; CURRENT APPLICATION NUMBER: US/09/245,041
; CURRENT PILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/093,630
; EARLIER PILING DATE: 1998-10-21
; EARLIER PILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: FastSEQ for Windows Version 3.0
125314 AAGTTCTAGGGTACATGTGCACAACGTGCAACTTTGTTACATATGTATACATGTGCCATG 125255
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US-09-358-055B-16/c
; Sequence 16, Application US/09358055B
; Patent No. 671327;
GENERAL INFORMATION:
; APPLICANT: Moore, K.
; APPLICANT: Moste, D.L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS INCLUDING; TITLE OF INVENTION: OBESITY
; FILE REFERENCE: 7853-151
; CURRENT PAPLICATION WUMBER: US/09/358,055B
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 09/245,041
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 99.6; DB 3;
Pred. No. 1.1e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3946 TGTTGGTGTGCTGCACCATTAACTC 3921
                                                                                                                                                                                                       125254 TTGGTATGCTGCACCCATTAACT 125232
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NAME/KEY: misc_feature
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US-09-949-016-14374/c
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ORGANISM: Human
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                             FEATURE:
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US-09-949-105-13276/c
US-09-949-105-13276, Application US/09949016
Sequence 13276, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                          4006 Traagritragggracargracacargcaggritrgriacarargratacarargcca 3947
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Patent No. 6727348
GENERAL INFORMATION:
APPLICANT: Moore, K.
APPLICANT: Nagle, D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
FILE REFERENCE: 7853-237
                                                                                                                                                                                    16 TITITITITITIGATGATITITAATAAAATATCATITITITITITITITIATTATACTT
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Pred. No. 1.1e-10;
0; Mismatches 29; Indels 0,
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80.1%; Pred. No. 1.1e-10;
tive 0; Mismatches 29; Indels
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CURRENT APPLICATION NUMBER: US/09/893,238
CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: 09/245,041
PRIOR FILING DATE: 1999-02-05
PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: 60/093,630
PRIOR APPLICATION NUMBER: 60/093,630
PRIOR APPLICATION NUMBER: 60/104,978
PRIOR PILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                      3946 TGTTGGTGTGCTGCACCCATTAACTC 3921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3946 TGTTGGTGTGCTGCACCCATTAACTC 3921
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                                                                                                   Query Match
Best Local Similarity 80.1%;
Matches 117; Conservative (
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Best Local Similarity 80.1<sup>3</sup>
Matches 117; Conservative
                   TYPE: DNA
CORGANISM: Homo sapiens
US-09-358-0558-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo sapiens
US-09-893-238-16
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LENGTH: 4072
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Sequence 14374, Application US/09949016

Sequence 14374, Application US/09949016

Patent No. 681339

GENERAL INCORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14374

LENGTH: 112623
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FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-3
PRIOR PILING DATE: 2000-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10261 TGCTGGTGCGCTGCACTAACTC 10236
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
| LOCATION: (1)...(100877)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13276
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14374
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Gaps

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Length 7384;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILTE OF INVENTION: 53 Human Secreted Proteins
FILTE OF INVENTION: 1870-167.
CURRENT APPLICATION NUMBER: US/09/984,429
CURRENT FILING DATE: 2000-110-30
PRIOR APPLICATION NUMBER: 09/248,143
PRIOR FILING DATE: 1999-04-08
PRIOR APPLICATION NUMBER: PCT/US98/21142
PRIOR APPLICATION NUMBER: PCT/US98/21142
PRIOR APPLICATION NUMBER: 60/061,463
PRIOR APPLICATION NUMBER: 60/061,463
PRIOR PILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
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PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION UNMBER: 60/061,532
PRIOR FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 727
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 455
LENGTH: 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-984-429-342/c
; Sequence 342, Application US/09984429
; Patent No. 7026447
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                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-429-455
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Best Local Similarity
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Best Local Similarity
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     57037 ACT-TTAAGTTTTTAGGGTACATGTGCACAATGTCCAGCTTAGTTACATATGTATACATGT 56979
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                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. 6943241e1 full length cDNA
TITLE OF INVENTION: NO. 6943241e1 full length cDNA
FILE REPERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARR: Patentin Ver. 2.1
SEQ ID NO 5250
LENGTH: 2829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 ACATGTGCCATGTTGGTTTGCTGCACCCATTAACTCA 185
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TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: PO108P2
CURRENT APPLICATION NUMBER: US/09/984,429
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/244,591
PRIOR APPLICATION NUMBER: 09/288,143
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1998-10-09
PRIOR FILING DATE: 1998-10-09
PRIOR FILING DATE: 1998-10-09
PRIOR APPLICATION NUMBER: 60/061,463
PRIOR APPLICATION NUMBER: 60/061,463
PRIOR APPLICATION NUMBER: 60/061,463
PRIOR APPLICATION NUMBER: 60/061,463
PRIOR APPLICATION NUMBER: 60/061,529
PRIOR PRILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
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                                                                                                                                                                  132 GCCATGCTGGTGTGCTGCACCCATTAACTC 161
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APPLICATION NUMBER: 60/061,527
FILING DATE: 1997-10-09
APPLICATION NUMBER: 60/061,536
                                                                                                                                                                                                                                                                                           RESULT 40
US-10-104-047-550
US-10-104-047-550
Sequence 550, Application US/10104047;
Patent No. 6943241;
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 77.13
Matches 121, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-550.
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Query Match
Best Local Similarity 82.4
Matches 126; Conservative
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ORGANISM: Homo sapiens
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US-09-949-016-12614/c
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APPLICANT: VERTER: J. Craig et al.

APPLICANT: VERTER: J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PEASEE for Windows Version 4.0

SEQ ID NO 15744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09818512
Sequence 3, Application US/09818512
Parent No. 6537780
GENERAL INCOMMATION:
GENERAL INCOMMATION:
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001192
CURRENT APPLICATION NUMBER: US/09/818,512
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50443 GTATACATGTGCCATGCTGCTGCTGCACCCACTAACTCA 50483
                                                                             160
                                                                                                                                                 RESULT 43
US-09-949-016-15744
; Sequence 15744, Application US/09949016
; Patent No. 6812339
                                                          TGCTGGTGTGCTGCACCCATTAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(116592)
CTHER INFORMATION: n = A,T,C or G
US-09-818-512-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Human
US-09-949-016-15744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 3
LENGTH: 116592
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Sequence 12614, Application US/09949016

Batent No. 6812339

Batent No. 6812339

Batent No. 6812339

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR PELING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR PELICATION NUMBER: 60/231,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: BEASLEY, Ellen et al.
APPLICANT: BEASLEY, Ellen et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CLOOL192DIV
CURRENT APPLICANTON NUMBER: US/10/354,065
CURRENT PLING DATE: 2003-01-30
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 116592
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Pred. No. 1.4e-10;
0; Mismatches 26; Indels 1;
Length 116592;
                                              26; Indels
Score 99.4; DB 3;
Pred. No. 1.4e-10;
0; Mismatches 26;
                                                                                                                                                                                                                                                                                                           48590 ACATGTGCCATGCTGGTGCGCTGCACCACTAA 48622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48590 ACATGTGCCATGCTGCTGCCCCCCCCCCACTAA 48622
                                                                                                                                                                                                                                                                  126 ACATGTGCCATGCTGGTGTGCTGCACCCATTAA 158
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                                                                                                                                                                                                                                                                                                                                                                                                US-10-354-065-3
; Sequence 3, Application US/10354065
; Patent No. 6884609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc_feature
; LOCATION: (1)...(116592)
; CTHEN INFORMATION: n = A,T,C or
US-10-354-065-3
  14.2%;
82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 82.4%;
Matches 126; Conservative
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RESULT 49

US-09-949-016-14577

Sequence 14577, Application US/09949016

Sequence 14577, Application US/09949016

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOL307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/21,758

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PSECSEQ for Windows Version 4.0

SEQ ID NO 14577

LENGTH: 678533
                                                                                                                                                     Sequence 13027, Application US/09949016

Sequence 13027, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOU307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-0-09-08

NUMBER OF SEQ ID NOS: 207012

SOFFWARE: FESSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30410 GGTACATGTGCACAATGTGCAGGTTAGTTACATATGTATACATGTGCCATGCTGGTGTGC 30351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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Best Local Similarity 88.1%; Pred. No. 1.6e-10;
Matches 119; Conservative 0; Mismatches 15; Indels
                                  213809 TGTACTGCACCCATTAACTC 213790
  142 TGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature; LCCATION: (1)...(45138); OTHER INFORMATION: n = A,T,C or G US-09-949-016-13027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30350 rGCACCCATTAACTC 30336
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                                                                                                                        RESULT 48
US-09-949-016-13027/c
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US-09-49-016-16061/c

Sequence 16061, Application US/09949016

Patch No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO3.07

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SSOFTWARE: PSELSEQ for Windows Version 4.0

LENGTH: 250958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163879 TTTAGGGTACATGTGCACAATGTGCAGGTTAGTTACATATGTATACATGTGCCATGCTGG 163820
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                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
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14.2%; Score 99.2; DB 3; Length 250958;
Best Local Similarity 86.4%; Pred. No. 1.6e-10;
Matches 121; Conservative 0; Mismatches 18; Indels 1;
                                                                                                                                                                                                                                                                                                                                                         Query Match
14.2%; Score 99.2; DB 3; Length 248968;
Best Local Similarity 86.4%; Pred. No. 1.6e-10;
Matches 121; Conservative 0; Mismatches 18; Indels 1;
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION UNMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12614
LENGTH: 248968
TYPE: DNA
TYPE: DNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163819 TGTACTGCACCCATTAACTC 163800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 TGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                      NAME/KEY: misc_feature

| LOCATION: (1)...(248968)

| OTHER INFORMATION: n = A,T,C or G

US-09-949-016-12641
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COTHER INFORMATION: n = A,T,C or G
US-09-949-016-16061
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LOCATION: (1)...(25095
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ORGANISM: Human
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Gaps

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Sequence 59510, Application US/09949016
; Sequence 59510, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
    CURRENT FILING DATE: 2000-04-14
    PRIOR APPLICATION NUMBER: 60/241,755
    PRIOR APPLICATION NUMBER: 60/231,768
    PRIOR FILING DATE: 2000-10-03
    PRIOR FILING DATE: 2000-10-03
    PRIOR FILING DATE: 2000-0-09-08
    NUMBER OF SEQ ID NOS: 207012
    NUMBER OF SEQ ID NOS: 207012
               APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 601;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.1%; Score 98.8; DB 3;
83.8%; Pred. No. 1.5e-10;
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83.8%; Pred. No. 1.5e-10;
live 0; Mismatches 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-59509
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ORGANISM: Human
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Patent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-14

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFFWARE: FASISEEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                 581007 TCATGTTGCTTTTTTTTTTTTTTTTTTTTTTTACTATTAGGAACTTTTATTATTATTA 581066
                                                                                                                                                                                                                                                                                                                           71 TACTITITAAGITITIAGGGTACATGTGCAAAGIGTGCAGGTTAGTTACATATATATACATG 130
                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                  DB 3; Length 678533;
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                                                                                                                                                                                               25; Indels
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Best Local Similarity 82.8%; Pred. No. 1.8e-10;
                                                                                                                                                Query Match

14.1%; Score 99; DB 3;
Best Local Similarity 82.8%; Pred. No. 1.8e-10;
Matches 125; Conservative 0; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                         S81126 TGCCATGCTGGTGTGCTGCACCCATTAACTC 581156
                                                                                                                                                                                                                                                                                                                                                                                                              TGCCATGCTGGTGTGCTGCACCCATTAACTC 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                          ; LOCATION: (1)...(678533)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | PEATURE:
| NAME/KEY: misc_feature
| LOCATION: (1)...(678533)
| OTHER INFORMATION: n = A,T,C or G
| US-09-949-016-14578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 125; Conservative
                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Human
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-949-016-14578
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US-09-949-016-59509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 14578
LENGTH: 678533
                                                                                                                                                                                                                                                                                                                                                                                                              131
                                                                                                                                                    Query Match
Best Local
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; Sequence 59509, Application US/09949016

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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 66524
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Best Local Similarity 78.7<sup>3</sup>
Matches 118<sup>7</sup>, Conservative
                                                                                                                                                                                                                                                                                                       Matches 118; Conservative
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                    ORGANISM: Human
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US-09-949-001-38/c
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LENGTH: 66525
                                                                                                                                                                                     US-09-949-001-32
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                                                                                                                                             TYPE: DNA
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Patent No. 6825336

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF;

FILE REPRENCE: CL000789

CURRENT APPLICATION VMDER: US/09/949,001

CURRENT APPLICATION VMBER: 06/231,323
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APPLICANT: Rosen et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE OF INVENTION: 53 Human Secreted Proteins
FILE OF INVENTION: 53 Human Secreted Proteins
FILE OF INVENTION NUMBER: US/09/984,429
CURRENT APPLICATION NUMBER: 09/244,591
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 1999-04-06
PRIOR FILING DATE: 1999-10-09
PRIOR FILING DATE: 1999-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,529
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,536
PRIOR FILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,536
PRIOR FILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,532
PRIOR PILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,532
PRIOR PILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,532
PRIOR PILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,532
PRIOR PILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
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PRIOR PILING DATE: 1997-10-09
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                                                                                        135 ATGCTGGTGTGCTGCACCCATTAACTCA 162
                                                                                                                       471 ATGCTGGTGCGCTGCACCCACTAACTCA 498
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Patent No. 7026447
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Matches 123, Conservative
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US-09-984-429-360/c
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Sequence 13828, Application US/09949016
Factor No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 38, Application US/09949001

Sequence 38, Application US/09949001

Patent No. 6825336

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF TILE REPRENCE: CL000789

CURRENT APPLICATION NUMBER: US/09/949,001

CURRENT PILING DATE: 2003-01-15

PRIOR APPLICATION NUMBER: 60/231,323

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ 1D NOS: 848

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                             18218 ATACTITAAGTITITAGGTACATGTGCACAATGTGCAGGTTAGTTACATATGTACATG 18159
                                                                                                                                                                                                                      71 TACTITIAAGTITITAGGGTACATGTGCAAAGTGTGCAGGTTAGTTACATATATACATG
                                                                                                           11 TAAAGTITITITITITIGAIGATTITIAATAAAATAICATTITCITITITITATTATTA
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  Length 66524;
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                                                     Indels
14.1%; Score 98.8; DB 3; 78.7%; Pred. No. 1.8e-10; iive 0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                              18158 TGACATGCTGGTGCGCTGCACCACTAACT 18129
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104954 TGTTGGTGTGCTGCACCCATTAACTC 104979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i LOCATION: (1)...(163181)
i OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 84.2*
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(16318:
                                                                                                              US-09-949-016-13730/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 163181
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LENGTH: 192700
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14.1%; Score 98.8; DB 4; Length 110096;
Best Local Similarity 84.2%; Pred. No. 1.9e-10;
Matches 123; Conservative 0; Mismatches 22; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INPORTATION:
APPLICANT: Horne, Darci T.
APPLICANT: Horne, Darci T.
APPLICANT: Cockley, Joseph G.
APPLICANT: Gone Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT APPLICATION NUMBER: US 60/211,379
PRIOR PILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-010-02
NUMBER OF SEQ ID NOS: 3950
NUMBER OF SEQ ID NOS: 3950
                                                                                                                                                                                                                                                                                                                                     Length 87323;
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US-09-880-107-1542
                                                                                                                                                                                                                                                                                                                               Ouery Match
14.1%; Score 98.8; DB 3;
Best Local Similarity 78.7%; Pred. No. 1.8e-10;
Matches 118; Conservative 0; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 GCCATGCTGGTGTGCTGCACCCATTAACTC 161
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-33
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ FOR Windows Version 4.0
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                   ; ORGANISM: Human
US-09-949-016-13828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 1542
LENGTH: 110096
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LENGTH: 87323
                                                                                                                                                                                                                                                  TYPE: DNA
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Sequence 13730, Application US/09949016

Sequence 13730, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
FILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/2241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
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TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-949-016-13477
                                                                                                                                                                                                                     SEQ ID NO 15419
LENGTH: 212449
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Sequence 1718.2. Application US/09949016

Patent No. 681239

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CLOOL3137
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-06

SOCTHARRE: FAST SOUTHAND
SEQ ID NOS: 207012

LENGTHARE: FAST SOUTHAND
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Patent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION UNMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
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                                                                                                                            1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.1%; Score 98.8; DB 3; Length 192704; 84.2%; Pred. No. 1.9e-10;
                                                    Score 98.8; DB 3; Length 192700;
Pred. No. 1.9e-10;
0; Mismatches 22; Indels 1;
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                                                       Query Match
Best Local Similarity 84.2%;
Matches 123; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 84.2
Matches 123; Conservative
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US-09-949-016-17182/c
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US-09-949-016-15419
US-09-949-016-11820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-949-016-17182
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Gequence 13477, Application US/09949016

Sequence 13477, Application US/09949016

Sequence 13477, Application US/09949016

Patent No. 6812339

CENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/2949,016

CURRENT FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

SPRIOR 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.1%; Score 98.8; DB 3;
84.2%; Pred. No. 1.9e-10;
tive 0; Mismatches 22;
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Pred. No. 1.9e-10;
0; Mismatches 22;
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ FOR Windows Version 4.0
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15419
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83.8%;
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Best Local Similarity 83.8<sup>3</sup>
Matches 124; Conservative
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Best Local Similarity 84.2'
Matches 123, Conservative
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NAME/KEY: misc_feature
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Gaps

Length 146401;

DB 3;

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Sequence 59511, Application US/09949016

Batent No. 681239
GENERAL INFORMATION:
TEREAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
FRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
FRIOR PILING DATE: 2000-10-03
FRIOR PILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 179319, Application US/09949016
Batent No. 6812319
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
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                                                                                                                        Score 98.6; DB 3; Length 1
Pred. No. 2e-10;
0; Mismatches 29; Indels
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14.1%; Score 98.4; DB 3; Length 6
Best Local Similarity 83.1%; Pred. No. 1.8e-10;
Matches 123; Conservative 1; Mismatches 22; Indels
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                                                                                                                           14.1%;
80.0%;
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Best Local Similarity 80.0
Matches 116; Conservative
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   ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16151
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ORGANISM: Human
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; Sequence 16151, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR PAPLICATION NUMBER: 60/241,755
; PRIOR PAPLICATION NUMBER: 60/241,768
; PRIOR PILING DATE: 2000-10-20
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FEAST EQ for Windows Version 4.0
; SEQ ID NO 16151
; LENGTH: 146401
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14.1%; Score 98.6; DB 5;
Best Local Similarity 92.0%; Pred. No. 1.8e-10;
Matches 104; Conservative 0; Mismatches 9;
                                                                                                                                           Sequence 398, Application US/09984429
Patent No. 7026447
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: PZ018P2
83021 ATGCTGGTGCGCTGCACCACTAACTCA 83048
                                                                                                                                                                                                                                                                                                                   THE KEFEKENCE FZOLDERZ

CURRENT PELICATION NUMBER: US/09/984,429

CURRENT FILING DATE: 2001-10-30

PRIOR PELING DATE: 2001-10-01

PRIOR FILING DATE: 2000-11-01

PRIOR FILING DATE: 1999-04-08

PRIOR FILING DATE: 1999-04-08

PRIOR FILING DATE: 1999-00-08

PRIOR FILING DATE: 1991-00-09

PRIOR FILING DATE: 1997-10-09

PRIOR FILING DATE: 1997-10-09

PRIOR PELING DATE: 1997-10-09

PRIOR PELING DATE: 1997-10-09

PRIOR FILING DATE: 1997-10-09
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TYPE: DNA
ORGANISM: Homo sapiens
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RESULT 68
US-09-949-016-16065
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US-09-949-016-13675
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LENGTH: 212139
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14.1%; Score 98.4; DB 5; Length 6407;
Best Local Similarity 90.6%; Pred. No. 2e-10;
Matches 116; Conservative 0; Mismatches 11; Indels 1
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Pred. No. 1.8e-10;
0; Mismatches 31; Indels
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GENERAL INFORMATION:
JULIE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: P2018P2
CURRENT APPLICATION NUMBER: US/09/984,429
CURRENT PILING DATE: 2001-10-30
FRIOR APPLICATION NUMBER: 60/244,591
FRIOR PILING DATE: 1999-04-08
FRIOR APPLICATION NUMBER: 09/288,143
FRIOR FILING DATE: 1999-04-08
FRIOR PILING DATE: 1999-10-08
FRIOR PILING DATE: 1997-10-09
FRIOR PILING DATE: 1997-10-09
FRIOR APPLICATION NUMBER: 60/061,463
FRIOR PILING DATE: 1997-10-09
FRIOR APPLICATION NUMBER: 60/061,529
FRIOR APPLICATION NUMBER: 60/061,529
FRIOR APPLICATION NUMBER: 60/061,529
FRIOR APPLICATION NUMBER: 60/061,536
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FRIOR APPLICATION NUMBER: 60/061,537
FRIOR APPLICATION NUMBER: 60/061,536
FRIOR FILING DATE: 1997-10-09
FRIOR APPLICATION NUMBER: 60/061,536
FRIOR FILING DATE: 1997-10-09
FRIOR FILING DATE: 1997-10-09
FRIOR APPLICATION NUMBER: 60/061,532
FRIOR FILING DATE: 1997-10-09
FRIOR FILING DATE: 1997-10-09
FRIOR FILING DATE: 1997-10-09
FRIOR FILING DATE: 1997-10-09
FRIOR APPLICATION NUMBER: 60/061,532
FRIOR APPLICATION NUMBER: 60/061,532
FRIOR FILING DATE: 1997-10-09
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FRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-00-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR FILING DATE: 2000-00-06
PRIOR FILING DATE: 2000-00-06
PRIOR FILING DATE: 2000-00-06
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1 Sequence 468, Application US/09984429

1 Patent No. 7026447

1 GENERAL INFORMATION:
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80.0%;
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Best Local Similarity 80.0°
Matches 128, Conservative
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US-09-984-429-468
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ORGANISM: Human
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Sequence 16065, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPRENCE: CLOU307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHWARE: FESTERQ for Windows Version 4.0
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Squence 13675, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

SPRIOR FILING DATE: 2000-10-03
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                                                                                                                                                                                                                                   Query Match
14.1%; Score 98.4; DB 3; Length 212139;
Best Local Similarity 82.2%; Pred. No. 2.3e-10;
Matches 125; Conservative 0; Mismatches 26; Indels 1;
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Sequence 12386, Application US/09949016

Patent No. 681239

GREEAL INFORMATION:

GREEAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 12386

LENGTH: 263693
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80.0%; Pred. No. 2.3e-10;
Ative 0; Mismatches 31; Indels
                                                                                                                                                            Score 98.4; DB 3; Length 23
Pred. No. 2.3e-10;
0; Mismatches 21; Indels
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                                                            | FEATURE:
| NAME/KEY: misc_feature
| LOCATION: (1) ... (235452)
| OTHER INFORMATION: n = A,T,C or G
| US-09-949-016-13675
                                                                                                                                                            Query Match
Best Local Similarity 84.7%;
Matches 122; Conservative
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Best Local Similarity 80.0
Matches 128; Conservative
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US-09-949-016-12386/c
                               TYPE: DNA
ORGANISM: Human
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; ORGANISM: Human
US-09-949-016-12386
SEQ ID NO 13675
LENGTH: 235452
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Sequence Sequence Sequence

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US-11-136-623-3 US-10-301-480-578850 US-10-301-480-1192259 US-11-121-086-51

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Sequence 1, Application US/10661966
; Publication No. US20050277118A1
; GENERAL INFORMATION:
; APPLICANT: Roth, Richard B.
; APPLICANT: Noth, Richard B.
; APPLICANT: Braun, Andreas
; TITLE OF INVENTION: OF MELANOMA AND TREATMENTS THEREOF
; TITLE OF INVENTION: OF MELANOMA AND TREATMENTS THEREOF
; FILE REFERENCE: 524592003800
; CURRENT APPLICATION NUMBER: US/10/661,966
; CURRENT PAPLICATION NUMBER: 60410,595
; PRIOR APPLICATION NUMBER: 60410,595
                                                                                                                                                                                                                                                                                                                                                                                                        US-10-304-113-4

US-10-304-113-4

US-10-027-632-267264

US-10-027-632-267265

US-10-027-632-267265

US-10-027-632-235941

US-10-027-632-235943

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US-10-027-632-256998
US-10-027-632-2569997
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US-10-301-480-91798
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US-09-764-869-1276
US-09-984-429-448
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'REMC_Celerra_SIDS3/pcodata/2/pubpna/US07_PUBCOMB.seq:*

'EMC_Celerra_SIDS3/pcodata/2/pubpna/US08_PUBCOMB.seq:*

'REMC_Celerra_SIDS3/pcodata/2/pubpna/US08_PUBCOMB.seq:*

'REMC_Celerra_SIDS3/pcodata/2/pubpna/US09B_PUBCOMB.seq:*

'REMC_Celerra_SIDS3/pcodata/2/pubpna/US09C_PUBCOMB.seq:*

'REMC_Celerra_SIDS3/pcodata/2/pubpna/US09C_PUBCOMB.seq:*

'REMC_Celerra_SIDS3/pcodata/2/pubpna/US10B_PUBCOMB.seq:*

'REMC_Celerra_SIDS3/pcodata/2/pubpna/US10B_PUBCOMB.seq:*

'REMC_Celerra_SIDS3/pcodata/2/pubpna/US10C_PUBCOMB.seq:*

'REMC_Celerra_SIDS3/pcodata/2/pubpna/US10C_PUBCOMB.seq:*

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'REMC_Celerra_SIDS3/pcodata/2/pubpna/US10F_PUBCOMB.seq:*

'REMC_Celerra_SIDS3/pcodata/2/pubpna/US11B_PUBCOMB.seq:*

'REMC_Celerra_SIDS3/pcodata/2/pubpna/US11B_PUBCOMB.seq:*

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'REMC_Celerra_SIDS3/pcodata/2/pubpna/US11B_PUBCOMB.seq:*
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Sequence 8028, Ap
Sequence 6776, Ap
Sequence 267263,
Sequence 72821,
Sequence 728921,
Sequence 728921,
Sequence 354, App
Sequence 354, App
Sequence 27, Appl
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Sequence 27, Appl
Sequence 27, Appl
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5875.235 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                          1 ctgtttcacataaagttttt.....gccttttaggtgatgtggca 700
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                 GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-719-993-6776

US-10-027-632-267263

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US-09-925-065A-728921

US-09-925-065A-728921

US-09-944-429-354

US-10-311-455-369

US-10-221-714A-27

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Maximum Match 100%
Listing first 70 summaries
                                                                                                                  - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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US-10-301-480-1184016 US-10-301-480-552761 US-10-301-480-1166170

US-10-301-480-705207 US-10-301-480-705208

ALIGNMENTS

US-10-330-773-76 US-10-301-480-570607

Sequence 235913, Sequence 235913, Sequence 235941, Sequence 235943, Sequence 235943, Sequence 219259, Sequence 214, Appl Sequence 214, Appl Sequence 214, Appl Sequence 218, Appl Sequence 218, Appl Sequence 218, Appl Sequence 11353, Appl Sequence 11353, Appl Sequence 11353, Appl Sequence 257167, Sequence 611, Appl Sequence 611, Appl Sequence 611, Appl Sequence 611, Appl Sequence 611, Appl Sequence 611, Appl Sequence 256997, Sequ

RISK

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TYPE: DNA
ORGANISM: Homo
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US-10-719-993-6776
                                                                                                US-09-764-891-8028
                                                      LENGTH: 19167
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; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICAMY: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFREENCE: PC006
; CHRENT APPLICATION UNMBER: US/09/764,891
; CURRENT PILING DATE: 2001-01-17
                                                                                                                                                                   Indels
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Pred. No. 4.5e-118;
1; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/422,344
PRIOR FILING DATE: 2002-10-29
NUMBER OF SEQ ID NOS: 61
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                       100.0%;
99.9%; F
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Matches 699; Conservative
                                                                                               ORGANISM: Homo sapiens
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US-09-764-891-8028/c
                                                                     LENGTH: 190276
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LOCATION: (1)...(100364)
COTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-7
US-10-719-993-6776
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30885
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- consult PALM or file wrapper
                                                                                                                                                                                                                                                                                                                        Score 109.2; DB 9; Length
Pred. No. 1.4e-09;
0; Mismatches 23; Indels
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CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55542
SOFTWARE: PASKEE for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6776, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
Prior application data removed
NUMBER OF SEQ ID NOS: 10231
SOFFWARE: PatentIn Ver. 2.0
SEQ ID NO 8028
                                                                                                                                                                                                                      Query Match
Best Local Similarity 82.3%;
Matches 130; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 84.2%;
Matches 123; Conservative
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ORGANISM: Homo sapiens
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US-10-027-632-267263/c
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Gaps

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395 AC-TITAAGTITIAGGGTACATGTGCACAAIGTGCAGKTTAGTTACATATGTATACATGT 337
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Sequence 728921, Application US/09925065A
Fublication No. US20040181048A1
GENERAL INFORMATION:
TERESTEL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: UNCleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-110-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
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                                                                                                                                                                                                                                                                                                                                                                                        Score 107; DB 7;
Pred. No. 6.5e-10;
1; Mismatches 91;
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 267263
LENGTH: 563
                                                                                                                                                                                                                                                                                                                                                                                        15.3%;
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Best Local Similarity 65.8
Matches 185; Conservative
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Matches 122, Conservative
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                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-267263
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Dolymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
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Pred. No. 6.5e-10;
1; Mismatches 91; Indels
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Polymorphisms in the Human Genome
                  THILE REFERENCE: 108827,129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 1000-03-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
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Sequence 267263, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
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APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
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65.8%;
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Best Local Similarity 65.8
Matches 185; Conservative
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ORGANISM: Human
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; ORGANISM: Homo sapiens US-09-984-429-354
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                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PELING DATE: 2000-10-24
PRIOR PELING DATE: 2000-10-24
PRIOR PELING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PELING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR PELING DATE: 2001-10-16
PRIOR PELING DATE: 2001-10-16
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
SPRIOR PELING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASTESQ for Windows Version 4.0
LENGTH: 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.3%; Score 107; DB 5; Length 596; 83.0%; Pred. No. 6.6e-10; ive 0; Mismatches 25; Indels
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Squence 354, Application US/09984429

Publication No. USZ0040010132A1

GENERAL INPORMATION:

APPLICANT: Rosen et al.

TILLE OF INVENTION: 53 Human Secreted Proteins

FILE REPERENCE: PZ018P2

CURRENT APPLICATION NUMBER: US/09/984,429

CURRENT FILING DATE: 2001-10-30

PRIOR FILING DATE: 2000-11-01

PRIOR APPLICATION NUMBER: 09/244,591

PRIOR APPLICATION NUMBER: 09/288,143

PRIOR APPLICATION NUMBER: PCT/US98/21142

PRIOR APPLICATION NUMBER: PCT/US98/21142

PRIOR APPLICATION NUMBER: 60/61,463

PRIOR FILING DATE: 1999-10-08

PRIOR FILING DATE: 1997-10-09
                                                                                        135 ATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                      445 ATGCTGGTGCTGCACCATTAACTC 471
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Publication No. US20050228172A9
GENERAL INFORMATION:
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US-09-925-065A-728921
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Matches 122; Conserv
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Sequence 369, Application US/10311455
; Sequence 369, Application US/10311455
; Publication No. US20030143606A1
; GRNERAL INFORMATION:
    APPLICANT: PIEPENBROCK, Christian
    APPLICANT: PIEPENBROCK, Christian
    APPLICANT: Diagnosis of Diseases Associated with the Immune System by Determi;
    TITLE OF INVENTION: Cytosine methylation
    FILE REFERENCE: 5013.1014
    CURRENT FILING DATE: 2002-12-16
    PRIOR FILING DATE: 2001-07-02
    PRIOR PILING DATE: 2001-06-30
    PRIOR APPLICATION NUMBER: DE 10043826.1
    PRIOR PILING DATE: 2000-06-30
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OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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Pred. No. 1.9e-09;
0; Mismatches 324; Indels
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Pred. No. 1.7e-09;
0; Mismatches 7;
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PRIOR APPLICATION NUMBER: 60/061,529
PRIOR FILING DATE: 1997-10-09
PRIOR PLING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/011,498
PRIOR APPLICATION NUMBER: 60/061,527
PRIOR APPLICATION NUMBER: 60/061,536
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 727
SEQ ID NO 354
LENGTH: 8766
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Best Local Similarity 49.0%;
Matches 312; Conservative (
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Best Local Similarity 94.1%;
Matches 111; Conservative
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APPLICANT: OLEX, Alexander
APPLICANT: OLEX, Alexander
APPLICANT: DIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
TITLE CP INVENTION: Muchod and nucleic acids for the analysis of astrocytomas
FILE REFERENCE: 5013.1013
CURRENT APPLICATION NUMBER: US/10/311,507
CURRENT APPLICATION NUMBER: PCT/EP01/07538
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PRIING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 95
LENGTH: 8666
                                              GTTATGTTGGTGTTTTTTTTTTTATTTA-TTATTTAGTATTAGGTATATTTTTAAT 1725
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        AAAGTTTTTTTTTTTTGATGATTTTAATAAAATATCATTTTCTTTTTTTATTATTAT 71
                                                                                        ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-507-95
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US-10-311-507-95
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TILE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: Lumor suppressor genes and oncogenes
FILE REFERENCE: 5013.1005
CURRENT APPLICATION NUMBER: US/10/221,714A
CURRENT APPLICATION NUMBER: DE 10013847.0
PRIOR APPLICATION NUMBER: DE 10013847.0
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-03-15
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SQ ID NOS: 540
SEQ ID NO 27
LENGTH: 8666
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ORGANISM: Artificial Sequence
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                                Sequence 477191, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
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US-09-925-065A-477191/c
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Sequence 207, Application US/10433793

Publication No. US20040142334A1

GENERAL INFORMATION:

APPLICANT: Epigenomics AG

TITLE OF INVENTION: Diagnose von mit Angiogenese assoziierten Krankheiten

FILE REFRENCE:

CURRENT APPLICATION NUMBER: US/10/433,793

CURRENT FILING DATE: 2003-06-06

NUMBER OF SEQ ID NOS: 212
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 Pred. No. 1.9e-09;
0; Mismatches 324; Indels
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49.08;
                 Matches 312; Conservative
 Best Local Similarity
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LENGTH: 8666
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GENERAL INCURRATION:
GENERAL INCURRATION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Uncleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108027.135
CURRENT APPLICATION NUMBER: US 60/243,096
FRIOR PELING DATE: 2000-10-24
PRIOR PELING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR PELING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PELING DATE: 2000-11-30
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-60
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 477191
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252 TAACTACTCTGATAAAAAGTTTTATAGTTTCCTACTTTTA
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                            Gaps
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-haq 92; Indels
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                        0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
RRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SEQ ID NO 477191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 477191, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
         Pred. No.
     65.8%;
                        Matches 185; Conservative
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Best Local Similarity 65.83
Matches 185; Conservative
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CORGANISM: Homo sapiens
US-09-925-065A-477191
       Best Local Similarity
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AC-TTTAAGTTTTAGGGTACATGTGCACAATGTGCAGTTTAGTTACATATGTATACATGT 272
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                                                                                                               Gaps
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Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICAMY: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
File Reference: 108827.128
CURRENT APPLICATION NUMBER: US/10/027,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 498;
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Pred. No. 1e-09;
0; Mismatches 92; Indels
149 TITCCIGITIAAAAIGTATIATICAAIGGITTAGIGITTIA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAACTACTCTGATAAAAAGTTTTATAGTTTCCTACTTTTA 292
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                                                                           , Sequence 267266, Application US/10027632; Publication No. US20020198371A1
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65.8%;
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Best Local Similarity 65.8
Matches 185; Conservative
                                                                                                          GENERAL INFORMATION:
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10-661966-1 146001-146700 a146311.rnpbm

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336 GCCATGCTGGTGTGCTGCACCCATTAACTC---GTCATTTAGCATTAGGTATATCTCCTA
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ITILE OF INVENTION: Identification and Mapping of Single Nucleotide
ITILE OF INVENTION: Identification and Mapping of Single Nucleotide
ITILE OF INVENTION: DOLYMORPHISMS in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/02/04.30
FRIOR FILING DATE: 2000-04-30
FRIOR FILING DATE: 2000-07-12
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR PRICATION NUMBER: US 60/195,218
FRIOR FILING DATE: 2000-02-24
FRIOR APPLICATION NUMBER: US 60/165,363
FRIOR PLING DATE: 1999-11-23
FRIOR APPLICATION NUMBER: US 60/156,358
FRIOR APPLICATION NUMBER: US 60/156,358
FRIOR APPLICATION NUMBER: US 60/156,358
FRIOR APPLICATION NUMBER: US 60/156,358
FRIOR APPLICATION NUMBER: US 60/156,358
FRIOR APPLICATION NUMBER: US 60/156,358
FRIOR APPLICATION NUMBER: US 60/156,358
FRIOR APPLICATION NUMBER: US 60/156,358
FRIOR PILING DATE: 1999-109-08
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Pred. No. 1.1e-09;
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Pred. No. 1.1e-09;
0; Mismatches 92
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 267262
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 267262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 267262, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
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65.8%;
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Best Local Similarity 65.8°
Matches 185; Conservative
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Best Local Similarity 65.8
Matches 185; Conservative
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US-10-027-632-267262
                                                                                                TYPE: DNA
ORGANISM: Human
                                                                            LENGTH: 563
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SEQUENCE 267262, Application US/10027632

SEQUENCE 267262, Application US/10027632

PUBLICANT US20020198371A1

GENERAL INFORMATION:
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE OF INVENTION: Polymorphisms in the Human Genome
FILE OF INVENTION: POlymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 1999-11-33

PRIOR FILING DATE: 1999-11-33

PRIOR FILING DATE: 1999-10-23

PRIOR PILING DATE: 1999-10-23

PRIOR PILING DATE: 1999-10-23

PRIOR PILING DATE: 1999-10-23

PRIOR PILING DATE: 1999-10-23

PRIOR FILING DATE: 1999-10-23

PRIOR FILING DATE: 1999-10-23

PRIOR PILING DATE: 1999-09-88
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                   Best Local Similarity 65.8
Matches 185; Conservative
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PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASESEQ for Windows Version 4.0
LENGTH: 563
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US-10-027-632-267265
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ORGANISM: Human
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                                                                                                                                  336 GCCATGCTGGTGCTGCACCCATTAACTC---GTCATTTAGCATTAGGTATATCTCCTA 280
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    GCCATGCTGGTGTGCTGCACCCATTAACTCACATGAAGTTTTTTAAATTTTAGTGACA 191
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                                            395 AC-TITAAGITITAGGGTACATGTGCACAATGTGCAGTTTAGTTACATATGTATACATGT
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Fublication No. US20020198371A1
GENERAL INFORMATION:
TTILE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: POlymorphisms in the Human Genome
FILE REFERENCE: 108877.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT PAPLICATION NUMBER: US 60/189,066
FRIOR FILING DATE: 2000-07-12
FRIOR FILING DATE: 2000-04-30
FRIOR FILING DATE: 2000-04-30
FRIOR FILING DATE: 2000-04-30
FRIOR FILING DATE: 2000-04-30
FRIOR FILING DATE: 2000-04-20
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-24
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Sequence 4, Application US/10304113

Sequence 4, Application US/10304113

Publication No. US20040102623A1

GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF PAKI EXPRESSION
FILE REFERENCE: RTS-0415
CURRENT APPLICATION NUMBER: US/10/304,113

CURRENT FILING DATE: 2002-11-23

NUMBER OF SEQ ID NOS: 167

LENGTH: 70043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: H. sapiens
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Best Local Similarity
Matches 126; Conserv
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-10-027-632-267264/c
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
FRIOR PAPLICATION NUMBER: US 60/198,676
FRIOR PILING DATE: 2000-07-12
FRIOR PILING DATE: 2000-04-20
FRIOR PILING DATE: 2000-03-29
FRIOR PILING DATE: 2000-03-29
FRIOR PAPLICATION NUMBER: US 60/195,218
FRIOR APPLICATION NUMBER: US 60/165,363
FRIOR APPLICATION NUMBER: US 60/157,363
FRIOR APPLICATION NUMBER: US 60/157,363
FRIOR APPLICATION NUMBER: US 60/157,363
FRIOR APPLICATION NUMBER: US 60/157,363
FRIOR APPLICATION NUMBER: US 60/157,363
FRIOR APPLICATION NUMBER: US 60/156,358
FRIOR APPLICATION NUMBER: US 60/156,358
FRIOR APPLICATION NUMBER: US 60/156,002
FRIOR APPLICATION NUMBER: US 60/156,002
FRIOR APPLICATION NUMBER: US 60/156,002
FRIOR APPLICATION NUMBER: US 60/156,002
FRIOR APPLICATION NUMBER: US 60/156,002
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Length 563;
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Score 105.4; DB 6;
Pred. No. 1.3e-09;
                                                                1; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 267265
LENGTH: 563
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; Sequence 267265, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/189,006
RIOR APPLICATION NUMBER: US 60/189,676
PRIOR FILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,368
PRIOR APPLICATION NUMBER: US 60/166,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-108-09
  192 GITTTAGICATTTTCCTAATTGAAAGTATCATAAGTAATCCATAAATTTGAAAAAATGT
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Pred. No. 1.3e-09;
1; Mismatches 92;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 267265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 24
US-10-027-632-235941/c
; Sequence 235941, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
                                                                                                                                                                                                                                                                                                Sequence 267265, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 65.5%;
Matches 184; Conservative
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                                                                                                                                                                                                                                                                                                                                                            336 GCCATGCTGGTGTGCTGCACCCATTAACTC---GTCATTTAGCATTAGGTATATCTCCTA 280
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                                                                                                                                      AATATTATATATATATTTAAAATGTATYATTATTCAATATTCTTTTTTTATTATTATTAT 396
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Publication No. US20030204075A9

Publication No. US20030204075A9

Publication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE OF INVENTION: Polymorphisms in the Human Genome

FILE OF INVENTION: Polymorphisms in the Human Genome

FILE SEPERENCE: 108627.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-109-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-08-28

PRIOR FILING DATE: 1999-08-28

PRIOR FILING DATE: 1999-08-28

PRIOR FILING DATE: 1999-08-28

PRIOR FILING DATE: 1999-08-28

PRIOR FILING DATE: 1999-08-28

PRIOR FILING DATE: 1999-08-28

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Pred. No. 1.3e-09;
1; Mismatches 92;
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Pred. No. 1.3e-09;
1; Mismatches 92
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Best Local Similarity 65.5%;
Matches 184; Conservative
  65.5%;
                            Matches 184; Conservative
     Best Local Similarity
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US-10-027-632-267264
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337

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251

396 131

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Best Local Similarity 72.9%;
Matches 148; Conservative
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                                                                                              ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-235942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 ATATATATATACATGCCATGCTGGTGCTGCACCCATTAACTCACATGAAGTTTTTTT 177
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Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/0218,006
PRIOR FILING DATE: 2002-04-30
PRIOR PELIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR PELIOR APPLICATION NUMBER: US 60/195,218
PRIOR PELIOR DATE: 2000-03-29
PRIOR PELIOR DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PELING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PELING DATE: 1999-109-28
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-8
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INVENTION: Identification and Mapping of Single Nucleotide INVENTION: Polymorphisms in the Human Genome
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Pred. No. 1.3e-09;
2; Mismatches 48;
                                 TILLE CF INCHILON: POLYMOTPDISMS IN the Hun CURRENT APPLICATION NUMBER: US/10/027,632 CURRENT FILING DATE: 2002-04-30 CURRENT FILING DATE: 2002-04-30 PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12 PRIOR PELING DATE: 2000-04-20 PRIOR FILING DATE: 2000-04-20 PRIOR FILING DATE: 2000-03-29 PRIOR PLING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: US 60/185,218 PRIOR FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: US 60/185,218 PRIOR FILING DATE: 1999-04-28 FRIOR FILING DATE: 1999-04-8 FRIOR FILING DATE: 1999-04-8 FRIOR FILING DATE: 1999-04-8 FRIOR FILING DATE: 1999-04-8 FRIOR FILING DATE: 1999-06-09 NUMBER OF SEQ. ID NOS: 325720 SECTION OF 235941
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72.9%;
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Best Local Similarity 72.9%
Matches 148; Conservative
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ORGANISM: Human
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282 ATATGTATACATGTGYCATGCTGATGTGCTGCACCCATTAACTCATTTASCATTAGGTAT 223
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-00-08

PRIOR FILING DATE: 1999-00-09

PRIOR FILING DATE: 1999-00-09

PRIOR FILING DATE: 1999-00-09

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-00-09

PRIOR FILING DATE: 1999-00-09

PRIOR FILING DATE: 1999-00-09

PRIOR FILING DATE: 1999-00-09

PRIOR FILING DATE: 1999-00-09

PRIOR FILING DATE: 1999-00-09

PRIOR FILING DATE: 1999-00-09

PRIOR PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002

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PRIOR APPLICATION NUMBER: US 60/146,002
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                                                                                                                                                                                                                                                                                                          2; Mismatches 48; Indels
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Pred. No. 1.3e-09;
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 235942
LENGTH: 600
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Publication No. US20020198371A1
GENERAL INFORMATION:
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US-10-027-632-235942
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Publication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REPERENCE: 108827.129

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2002-04-30

PRIOR FILING DATE: 2000-07-20

PRIOR PELING DATE: 2000-07-20

PRIOR PELING DATE: 2000-03-24

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

PRIOR PRIOR PRICE TION NUMBER: US 60/146,002

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Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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Best Local Similarity 72.9°
Matches 148; Conservative
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US-10-027-632-235941/c
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282 ATATGTATACATGTGYCATGCTGATGTGCTGCACCCATTAACTCATTTASCATTAGGTAT 223
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Pred. No. 1.3e-
2; Mismatches
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR FILING DATE: 2002-04-30
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR PLICATION NUMBER: US 60/198,676
PRIOR PAPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR PRILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTERED FOR WINDOWS VERSION 4.0
SOFTWARE: 600
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72.9%;
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Matches 148; Conservative
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US-10-027-632-235943/c
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TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: CLOGOLOG-CIPCON
CURRENT APPLICATION NUMBER: US/11/136,623
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: 09/730,002
PRIOR PILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SCOTUN 03-82938
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US-10-301-480-578850
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                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Human
US-11-136-623-3
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NAME/KEY:
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| Sequence 3, Application US/09918657
| Publication No. US20030077773A1
| Sequence 3, Application No. US20030077773A1
| Sequence 3, Application No. US20030077773A1
| GENERAL INFORMATION: SOLATED HUMAN TRANSPORTER PROTEINS, TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS, TITLE OF INVENTION: AND USES THEREOF
| FILE REFERENCE: CLO01006-CIP | CURRENT APPLICATION NUMBER: US/09/818,657 | CURRENT APPLICATION NUMBER: 09/730,002 | PRIOR FILING DATE: 2001-12-06 | NUMBER OF SQL ID NOS: 4 | NUMBER OF SQL ID NOS: 4 | SOCTWARE: FRSENCE: FROM THE NUMBER OF SQL ID NOS: 4 | SOCTWARE: FRSENCE | SOCTOR IN INCOME. | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCTWARE: FRSENCE | SOCT | SOCTWARE: FRSENCE | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOCT | SOC
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US-11.136-623-3/C
Sequence 3, Application US/11136623
Sequence 3, Application No. US20050221437A1
SEMENAL INFORMATION:
APPLICANT: BRANDON, Rhonda, et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 6.6e-09;
0; Mismatches 26; Indels 0;
                                                                                                                                           15.1%; Score 105.4; DB 7; Length 600; 72.9%; Pred. No. 1.3e-09; ive 2; Mismatches 48; Indels 5
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82.3%;
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Best Local Similarity 72.9
Matches 148; Conservative
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Best Local Similarity 82.33
Matches 121; Conservative
                        ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-235943
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ORGANISM: Human
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LENGTH: 600
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SEQ ID NO 3
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Sequence 578850, Application US/10301480

Dublication No. US2066055564A1

Dublication No. US20660055564A1

Dublication No. US20660055564A1

APPLICANT: Wang, David G.

TITLE OF INVENTION: In the Human Genome

TITLE OF INVENTION: In the Human Genome

FILE REPRENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT PILING DATE: 2002-11-21

PRIOR FILING DATE: 2002-08-09

PRIOR FILING DATE: 2002-08-09

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FastSEQ for Windows Version 4.0

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179,
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214,
226,
   Score 105.4; DB 13; Length 82938;
Pred. No. 6.6e-09;
0; Mismatches 26; Indels 0;
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213,
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166,
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162,
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161,
173,
185,
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208,
220,
232,
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NAME/KEY: misc_feature
LOCATION: 238, 239, 240, 241, 242,
OTHER INFORMATION: n = A,T,C or G
   15.1%;
82.3%;
Query Match
Best Local Similarity 82.3
Matches 121; Conservative
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ORGANISM: Homo sapien
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14.9%;
80.8%;
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SOFTWARE: Patentin version 3.3
SEQ ID NO 51
LENGTH: 176760
TYPE: DNA
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87.5%;
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Best Local Similarity 87.5°
Matches 126; Conservative
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Matches 122, Conservative
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US-11-121-086-51
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US-10-322-281-214
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               RESULT 34
US-11-121-086-51
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Publication No. US20060057564A1

GENERAL INPORMATION:

TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms

TITLE OF INVENTION: 10 the Human Genome

TITLE OF INVENTION: 10 the Human Genome

FILE REPRENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT APPLICATION NUMBER: US 10/215,598

PRIOR FILING DATE: 2002-08-09

PRIOR FILING DATE: 2002-08-09

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: PRESEQ FOR WINGOWS Version 4.0

SEQ ID NO 1192259

LENGTH. 989
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213, 214,
225, 226,
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Best Local Similarity 79.1%; Pred. No. 1.7e-09;
Matches 125; Conservative 0; Mismatches 33; Indels 0;
                 Indels
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208, 209, 210, 2
220, 221, 222, 2
232, 233, 234, 2
Pred. No. 1.7e-09;
0; Mismatches 33;
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163,
175,
187,
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LOCATION: 114, 145, 146, 147, 148, 149, 150, 151
LOCATION: 186, 157, 158, 159, 160, 161, 162, 163
LOCATION: 168, 169, 170, 171, 172, 173, 174, 175
LOCATION: 180, 181, 182, 183, 184, 185, 186, 187
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: 203, 204, 205, 206, 207, 208, 209, 210
LOCATION: 213, 216, 217, 218, 219, 220, 221, 222
LOCATION: 227, 228, 229, 230, 231, 232, 233, 234
OTHER INFORMATION: n = A,T,C or G
                 0; Mismatches
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) LOCATION: 238, 239, 240, 241, 242, 243

) OTHER INFORMATION: n = A,T,C or G

US-10-301-480-1192259
79.1%;
                 Conservative
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ORGANISM: Homo sapien
Best Local Similarity
Matches 125; Conserv
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US-10-301-480-1192259
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APPLICANT: POULSEN, KIRSTEN V.
TITLE OF INVENTION: WUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.600-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 05.05-05-07
PRIOR FILING DATE: 2004-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 15; Length 176760;
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Pred. No. 8.9e-09;
0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REPERENCE: 229452001000
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Indels
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Pred. No. 1.1e-08;
0; Mismatches 17
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Sequence 51, Application US/11121086 Publication No. US20050266459A1 GENERAL INFORMATION:
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Sequence 56441, Application US/10301480

Publication No. US20060057564A1

Publication No. US20060057564A1

Publication No. US20060057564A1

APPLICANT: Wang, David G.

TITLE OF INVENTION: in the Human Genome

TITLE OF INVENTION: in the Human Genome

FILE REFERENCE: 108027.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT FILING DATE: 2002-11-21

PRIOR FILING DATE: 2002-08-09

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 599
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Sequence 1177850 Application US/10301480

Bublication No. US20660657564A1

GENERAL INPORMATION:
TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137

CURRENT APPLICATION WUMBER: US/10/301,480

CURRENT FILING DATE: 2002-11-21

PRIOR APPLICATION WUMBER: US 60/311,695

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION WUMBER: US 60/311,695

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12;
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86.9%; Pred. No. 2.2e-09;
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                     586372 TGCTGCACCCATTAACTCA 586390
144 TGCTGCACCCATTAACTCA 162
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ORGANISM: Homo sapien
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                                                                                                    RESULT 38
US-10-301-480-564441/c
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LOCATION: (1)...(1790242)

OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-

US-10-719-993-6940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-719-993-6940

Sequence 6940, Application US/10719993

Publication No. US20040265849A1

Publication No. US20040265849A1

APPLICANT: CARGILL, Michale et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: ALZHRIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001496

CURRENT APPLICATION NUMBER: US/10/719,993

CURRENT FILING DATE: 2003-11-24

NUMBER OF SEQ ID NOS: 55342

SOFTWARE: Feat-SEQ for Windows Version 4.0

LENGTH: 1790242
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                                                                                                            APPLICANT: Aziz, Natasha
APPLICANT: Aziz, Natasha
APPLICANT: Aziz, Natasha
APPLICANT: Zizonik, Albert
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITITIE OF INVENTION: NOVEL METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER FILE REFERENCE: file
CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARE: Patentin version 3.2
SEQ ID NO 3.1
LENGTH: 126882
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Pred. No. 1.1e-08;
0; Mismatches 29; Indels 0; G
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                                                    Sequence 321, Application US/10756149
Publication No. US20050181375A1
GENERAL INFORMATION:
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Best Local Similarity 89.24
Matches 124; Conservative
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US-10-756-149-321
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                                JS-10-756-149-321
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Best Local (
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Publication No. US20020182586A1
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                                                                                                                              241 TAAGTITITAGGGTACATGTGCACAATGTGCAGGTTAGTTACATATGTATACATGTGCCAT 182
   92
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Sequence 469, Application US/09984429
Publication No. US20040010132A1
GENERAL INFORMATION:
TITLE OF INVENTION: 53 Human Secreted Proteins
FILER REFERENCE: PZ018P2
CURRENT FILING DATE: 2001-10-30
PRIOR PILING DATE: 2001-11-01
PRIOR PLING DATE: 2001-11-01
PRIOR PLING DATE: 1999-04-08
PRIOR PLING DATE: 1999-06
PRIOR PLING DATE: 1999-06
PRIOR PLING DATE: 1999-10-09
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LOCATION: (7234)..(7234)
OTHER INFORMATION: n equals a,t,g, or c
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RESULT 41 US-10-087-192-238/c ; Sequence 238, Application US/10087192

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114373 TTTTTTTTTTTTTTTTTTTTTTTTTAGGTTTTTAGGGTACATGTGCACATGTGCAGG 114314
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Publication No. US20050266459A1
Sequence 98, Application US/11121086
Publication No. US20050266459A1
SAPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: OUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
SHORE FILING DATE: 2004-05-04
SHORE FILING DATE: 2004-05-04
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GENERAL INPORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000.122
CURRENT APPLICATION WUMBER: US 10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR PELLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FASAESO FOR WINDOWS VERSION 4.0
SEQ ID NO 238
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Pred. No. 1.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

14.9%; Score 104; DB 6;
Best Local Similarity 95.5%; Pred. No. 1.4e-08;
Matches 107; Conservative 0; Mismatches 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1) ___.(127369)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin version 3.3
SEQ ID NO 98
LENGTH: 171732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 83.3%;
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-11-121-086-98
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
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NAME/KEY: Unsure
LOCATION: (14335)..(14434)
OTHER INFORMATION: n = any nucleic acid
                                                                                                                                                             NAME/KEY: Unsure
LOCATION: (16247)..(16346)
OTHER INFORMATION: n = any nucleic acid
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LOCATION: (59749)..(59755)
OTHER INFORMATION: n = any nucleic acid
FEATURE:
NAME/KEY: misc_feature
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LOCATION: (59744)..(59744)
OTHER INFORMATION: n = any nucleic acid
FERTURE:
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LOCATION: (36774)..(36873)
OTHER INFORMATION: n = any nucleic acid
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LOCATION: (59740)..(59740)
OTHER INFORMATION: n = any nucleic acid
FEAPURE:
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LOCATION: (59742)..(59742)
OTHER INFORMATION: n = any nucleic acid
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LOCATION: (36432)..(36433)
OTHER INFORMATION: n is a, c, g, or t
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LOCATION: (59740)..(59740)
OTHER INFORMATION: n is a, c, g, or
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NAME/KEY: misc feature
LOCATION: (36774): (36873)
OTHER INFORMATION: n is a, c, g, or
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NAME/KEY: misc_feature
CCCATION: (59742)..(59744)

THER INFORMATION: n is a, c, g, or
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LOCATION: (36293)..(36298)
OTHER INFORMATION: n is a, c, g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (36314)..(36314)
OTHER INFORMATION: n is a, c, g,
                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (16247). (16346)
OTHER INFORMATION: n is a, c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (17457). (17457)
OTHER INFORMATION: n is a, c
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LOCATION: (21818)..(21818)
OTHER INFORMATION: n is a,
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NAME/KEY: misc_feature
LOCATION: (36316)..(36316)
OTHER INFORMATION: n is a,
                                                                                 NAME/KEY: misc feature
LOCATION: (14335)..(14434)
OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                      WESUL 43
Sequence 19, Application US/10517905
Sequence 19, Application US/10517905
Sequence 19, Application US/10517905
Sequence 19, Application US/10517905
Sequence 19, Application Wesucoo084142A1
Sequence 19, Application Wesucoo084142A1
SEQUENCE INCOMATION:
APPLICANT: Michael, Heinrich Charles
APPLICANT: Demetri, George D.
TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR
TITLE OF INVENTION: ACHHA (PDGFRA) AS DIAGMOSTIC MARKERS AND THERAPEUTIC TARGETS
TILE REFERENCE: 899-65892-02
CURRENT FILING DATE: 2004-12-10
PRIOR APPLICATION NUMBER: US 60/389,107
PRIOR FILING DATE: 2003-01-08
SOFTWARE PAPLICATION NUMBER: US 60/389,899
PRIOR FILING DATE: 2003-01-08
SOFTWARE PATENTIN WEST SOR 27
SOFTWARE PATENTIN VERSION 3.2
SEQ ID NO 19
LENGTH: 191150
39078 ACATGTGCCATGCTGTGCTGCACCCATTAACTC 39113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: n = any nucleic acid FEATURE:
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LOCATION: (10577)..(10676)
OTHER INFORMATION: n is a, c, g, or t
FRATURE:
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LOCATION: (10577)..(10676)
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(8978)..(166510)
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(8697)..(8787)
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LOCATION: (2331)..(2648)
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(4903)..(5163)
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COCATION: (6286)..(8524)
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(8525)..(8696)
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(2649)..(4902)
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(5164)..(6154)
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(6155)..(6285)
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(8788)..(8977)
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ORGANISM: Homo sapiens
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LOCATION: (50)..(2330)
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LOCATION: (1)..(49)
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NAME/KEY: I
LOCATION: (
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LOCATION:
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NAME/KEY:
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LOCATION:
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LOCATION:
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MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 102980;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17645, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DET
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FagtSEQ for Windows Version 4.0
                                                                                                                                                                             Sequence 1330, Application US/10087192
| Publication No. US20020182586A1
| GENERAL INFORMATION:
| APPLICANT: MOTEL OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF USERS OF US
35311 ACATGTGCCATGCTGTGTGCTGCACCCATTAACTC 35276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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                                                                                                                            RESULT 44
US-10-087-192-1330/c
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US-10-741-600-17645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 ACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                        NAME/KEY: Unsure
LOCATION: (59759)..(59760)
OTHER INFORMATION: n = any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Unsure
LOCATION: (82745)..(82844)
OTHER INFORMATION: n = any nucleic acid
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LOCATION: (96508)..(96607)
OTHER INFORMATION: n = any nucleic acid
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LOCATION: (157152)..(157251)
OTHER INFORMATION: n = any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (59776)..(59875)
OTHER INFORMATION: n = any nucleic acid
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LOCATION: (161475)..(161574)
OTHER INFORMATION: n is a, c, g, or t
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LOCATION: (59776)..(59875)
OTHER INFORMATION: n is a, c, g,
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LOCATION: (147675)..(147774)
OTHER INFORMATION: n is a, c,
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NAME/KRY: misc_feature
LOCATION: (157152). (157251)
OTHER INFORMATION: n is a, c,
      LOCATION: (59749)..(59755)
OTHER INFORMATION: n is a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (82745)..(82844)
OTHER INFORMATION: n is a, c,
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THER INFORMATION: n is a, c,
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LOCATION: (147675)..(147774)
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LOCATION: (59759)..(59760)
OTHER INFORMATION: n is a,
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LOCATION: (59765)..(59766)
OTHER INFORMATION: n is a,
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LOCATION: (96508)..(96
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Sequence 1190576, Application US/10301480
; Sequence 1190576, Application US/10301480
; Sequence 1190576, Application US/10301480
; GENERAL INFORMATION: US20060057564A1
; TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT PAPLICATION NUMBER: US/10/301,480
; PRIOR APPLICATION NUMBER: US 60/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastsEQ for Windows Version 4.0
; SEQ ID NO 1190576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09949654
Patent No. US2002127644A1
Fatent No. US2002127644A1
Fatent No. US200212764A1
FAPELICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REPERBNCE: CLOO0917
CURRENT APPLICATION NUMBER: US/09/949,654
CURRENT APPLICATION NUMBER: 00/231,572
                                                                                                                                                                                                                      694
                                                                                                                                                                                                                                                                 695 TATTATATATATACTTTAAGGTACATGTGCACAATGTGCAGGTTAGTACATATGT 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 TITCACATAAAGTITITITITITITITITAATAAAATATCATTITTITATT
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                                                                                 Length 987;
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                                                                             Score 103.6; DB 12; Length
Pred. No. 3.3e-09;
0; Mismatches 34; Indels
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                                                                                                                                                                                                                                                                                                                                                                                     755 ATACATGTGCCATGCTGTGCTGCTGCACCCATTAACTC 792
                                                                                                                                                                                                                                                                                                                                                          124 ATACATGCCATGCTGGTGTGCTGCACCCATTAACTC 161
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                                                                             Query Match
Best Local Similarity 78.5%;
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 78.5
Matches 124; Conservative
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; ORGANISM: Homo sapien
US-10-301-480-1190576
            ; ORGANISM: Homo sapien
US-10-301-480-577167
                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 48
US-10-301-480-1190576
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Sequence 577167, Application US/10301480

Publication No. US20060057564A1

GENERAL INFORMATION:

JENERAL INFORMATION:

TITLE OF INVENTION: In the Human Genome

TITLE OF INVENTION: in the Human Genome

TITLE OF INVENTION: in the Human Genome

TITLE OF INVENTION: in the Human Genome

FILE REFERENCE: 108827.137

CURRENT FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 10/215,598

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR PILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SEQ ID NO 577167

LENGTH: 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)...(103660)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13253
52865 AGITITIAGGGTACATGTGCACATGTGCAGGTTAGTTACATATGTATACATGTGCCATGC 52924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52806 TTTTTTTTTTTTTTGAAATGGAGTTTCAGTCTCTTTTTTTATTATTATTATATA 52864
                                                                                                                                                                                                                                                                                                                      Sequence 13253, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDILOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 AGTITIAGGGTACAIGTGCAAAGTGTGCAGGTTAGTTACATATATATATAGGGCATGC
                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.8%; Score 103.8; DB 10; Length 103660; llarity 87.4%; Pred. No. 1.4e-08; Conservative 0; Mismatches 17; Indels 1; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 13253
                                                                                                                                                                                         52925 TGGTGTACCGCACCCATTAACTC 52947
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Best Local Similarity
Matches 125; Conserv
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RESULT 52
US-10-074-095-661/c
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                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                            Length 368004;
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0
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
                                                                                                                                                                                          Ouery Match
14.8%; Score 103.6; DB 3;
Best Local Similarity 21.6%; Pred. No. 2.3e-08;
Matches 130; Conservative 0; Mismatches 473;
PRIOR FILING DATE: 2000-09-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12101, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
                                                                                                    FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(368004)
OTHER INFORMATION: n = A,T,C or G
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                                                                        TYPE: DNA
ORGANISM: Human
                                         SEQ ID NO 3
LENGTH: 368004
                                                                                                                                                             US-09-949-654-3
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LOCATION: (2305)..(2955)
OTHER INFORMATION: 86% homologous to Homo sapiens putative p150, accession number OTHER INFORMATION: U93574, Smith-Waterman Score=1034.
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                                                                                                                                                                                                                                                                                                                                                   Length 3200;
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Batent No. US20020094953A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC008
CURRENT APPLICATION NUMBER: US/09/764,860

CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1198
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                           16; Indels
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Pred. No. 1.1e-08;
0; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                     Score 103.4; DB 1
Pred. No. 5.3e-09;
0; Mismatches 16
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
LENGTH: 3200
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Local Similarity 87.6%;
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                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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                                                                                                                                                                                                                  FEATURE:
NAME/KEY: SIMILAR
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US-09-764-860-661/c
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R FILING DATE: 2000-12-08
R APPLICATION NUMBRR: 60/229,344
R FILING DATE: 2000-09-01
R FILING DATE: 2000-09-01
R FILING DATE: 2000-09-05
R FILING DATE: 2000-09-01
R APPLICATION NUMBER: 60/229,343
R FILING DATE: 2000-09-01
R APPLICATION NUMBER: 60/229,345
R FILING DATE: 2000-09-01
R APPLICATION NUMBER: 60/229,287
R FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFILING DATE: 2000-10-02

RR APPLICATION NUMBER: 60/237,040

RR APPLICATION NUMBER: 60/240,960

RR APPLICATION NUMBER: 60/240,960

RR APPLICATION NUMBER: 60/239,935

RR APPLICATION NUMBER: 60/239,935

RR APPLICATION NUMBER: 60/239,937

RR PILING DATE: 2000-10-13

RR PILING DATE: 2000-10-13

RR PILING DATE: 2000-10-13

RR PILING DATE: 2000-10-20

RR PILING DATE: 2000-10-20

RR PILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                 R APPLICATION NUMBER: 60/236,367
R FILING DATE: 2000-09-29
R APPLICATION NUMBER: 60/237,039
R PILING DATE: 2000-10-02
R APPLICATION NUMBER: 60/237,038
R FILING DATE: 2000-10-02
R APPLICATION NUMBER: 60/236,370
R APPLICATION NUMBER: 60/236,370
R APPLICATION NUMBER: 60/236,802
R APPLICATION NUMBER: 60/236,802
R APPLICATION NUMBER: 60/236,802
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R FILING DATE: 2000-11-08
R APPLICATION NUMBER: 60/249,216
R FILING DATE: 2000-11-17
R FILING DATE: 2000-11-17
R FILING DATE: 2000-11-17
R PILING DATE: 2000-11-17
               APPLICATION NUMBER: 60/251,868
FILING DATE: 2000-12-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,213
FILING DATE: 2000-11-17
                                                                                                                                                                                           APPLICATION NUMBER: 60/229,513
FILING DATE: 2000-09-05
APPLICATION NUMBER: 60/231,413
FILING DATE: 2000-09-06
                                                                                                                                                                                                                                          FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/229,509
FILING DATE: 2000-09-05
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APPLICATION NUMBER: 60/225,759
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FILING DATE: 2000-09-27
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FILING DATE: 2000-10-02
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APPLICATION NUMBER: 60/225,213
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APPLICATION NUMBER: 60/225,214
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R PELLING DATE: 2000-08-14
R FILING DATE: 2000-07-26
R APPLICATION NUMBER: 60/241,809
R APPLICATION NUMBER: 60/241,809
R APPLICATION NUMBER: 60/249,299
R FILING DATE: 2000-10-17
Sequence 661, Application US/10074095
Publication No. US20030077704A1
GENERAL INFORMATION:
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FILING DATE: 2000-09-29
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FILING DATE: 2000-09-29
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FILING DATE: 2000-09-29
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FILING DATE: 2000-10-20
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FILING DATE: 2000-11-01
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APPLICATION NUMBER: 60/251,856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 24132;
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APPLICANT: David W. Morris
APPLICANT: David W. Morris
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REPRENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330, 773
CURRENT FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 991
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                               APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC008C2
CURRENT APPLICATION NUMBER: US/10/212,872
CURRENT FILING DATE: 2002-08-07
Prior application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 1198
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 661
LENGTH: 24132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Pred. No. 1.1e-08;
0; Mismatches 23;
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                     Sequence 661, Application US/10212872
Publication No. US20030215893A1
GENERAL INFORMATION:
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Best Local Similarity 83.67
Matches 117; Conservative
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Matches 117; Conservative
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                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-10-212-872-661
US-10-212-872-661/c
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US-10-330-773-76/c
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PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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R FILING DATE: 2000-11-17
R FILING DATE: 2000-11-17
R R FILING DATE: 2000-11-17
R APPLICATION NUMBER: 60/249,264
R R FILING DATE: 2000-11-17
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R R FILING DATE: 2010-11-17
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R APPLICATION NUMBER: 60/249,207
R FILING DATE: 2000-11-17
R APPLICATION NUMBER: 60/249,245
R FILING DATE: 2000-11-17
R APPLICATION NUMBER: 60/249,245
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APPLICATION NUMBER: 60/231,242
FILING DATE: 2000-09-08
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APPLICATION NUMBER: 60/249,217
FILING DATE: 2000-11-17
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RESULT 53

RESULT 55 US-10-301-480-570607

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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
CURRENT FILING DATE: 2002-10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 987
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IITLE OF INVENTION: In the Human Genome
TITLE OF INVENTION: In the Human Genome
TITLE OF INVENTION: In the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-00
SEQ ID NOS: 1226818
SOFTWARE: FREEEEQ for Windows Version 4.0
SEQ ID NO 1166170
LENGTH: 987
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82.5%; Pred. No. 4.2e-09;
tive 0; Mismatches 25;
                                                    772 ATGCTGGTGCTGCACCCACTAACTC 798
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                                                                                                                         RESULT 57
US-10-301-480-552761/c
'Sequence 552761, Application US/10301480
'Publication No. US20060057564A1
'GENERAL INFORMATION:
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ORGANISM: Homo sapien
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; ORGANISM: Homo sapien
US-10-301-480-1166170
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US-10-301-480-1166170/c
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Sequence 570607, Application US/10301480

Publication No. US200600575641

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms;

TITLE OF INVENTION: In the Human Genome

FILE REFERENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

PRIOR APPLICATION NUMBER: US 10/215,598

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR APPLICATION NUMBER: US 60/311,695

SPRIOR FILING DATE: 2001-08-09

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: In the Human Genome
FILE REPERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT APPLICATION NUMBER: US/10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 865
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Pred. No. 4.1e-09;
0; Mismatches 20;
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Best Local Similarity 85.7%;
Matches 126; Conservative (
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Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapien
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US-10-301-480-1184016
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14.7%; Score 102.8; DB 7; Length 729;
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Best Local Similarity 81.5%;
Matches 119; Conservative
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US-10-027-632-256997/c
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; ORGANISM: Human
US-10-027-632-256998
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Tedentification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108027.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-07-12
PRIOR PELING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 1000-02-24
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-10-24
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTERE OF Windows Version 4.0
SEQ ID NO 256997
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Publication No. US20020198371A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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Best Local Similarity 81.5%; Pred. No. 4.2e-09;
Matches 119; Conservative 0; Mismatches 27
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Publication No. US20020198371A1
GENERAL INFORMATION:
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
ITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
FRIOR PELICATION NUMBER: US 60/218,006
PRIOR PLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-07-329
PRIOR FILING DATE: 2000-03-29
PRIOR PLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR PLICATION NUMBER: US 60/167,363
PRIOR PLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR PLING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PASSEE OF WINDOWS VEFSION 4.0
SEQ ID NO 256997
LINGUAL TO 256997
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Pred. No. 4.2e-09;
0; Mismatches 27
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
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Publication No. US20030204075A9
GENERAL INFORMATION:
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TITLE OF INVENTION: in the Human Genome FILE REFERENCE: 108827.137 CURRENT APPLICATION NUMBER: US/10/301,480 CURRENT FILING DATE: 2002-11-21 PRIOR APPLICATION NUMBER: US 60/311,695 PRIOR FILING DATE: 2002-08-09 PRIOR FILING DATE: 2001-08-10 NUMBER OF SEQ ID NOS: 1226818 SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO91798 LENGTH: 729
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
ITTLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT PILING DATE: 10802.04-30
FRIOR PILING DATE: 2000-07-12
PRIOR PLING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-20
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 1900-03-29
PRIOR FILING DATE: 1909-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
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PRIOR FILING DATE: PARENCENTON NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-05
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Matches 119; Conservative 0; Mismattre
  4.2e-09;
ches 27; Indels
                           0; Mismatches
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    Pred. No.
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                        Matches 119; Conservative
    Best Local Similarity
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US-10-027-632-256998/c
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US-10-027-632-256998
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APPLICANT: Wang, David G. TILLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms

US-10-301-480-91798/c 'Sequence 91798, Application US/10301480 ; Publication No. US20060057564A1 ; GENERAL INFORMATION:

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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FASISEQ for Windows Version 4.0
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Pred. No. 4.2e-09;
0; Mismatches 27; Indels
                                                                      Query Match 14.7%; Score 102.8; DB 12; Best Local Similarity 81.5%; Pred. No. 4.2e-09; Matches 119; Conservative 0; Mismatches 27;
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; Sequence 91799, Application US/10301480
; Publication No. US20060057564A1
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Best Local Similarity 81.5%;
Matches 119; Conservative
; ORGANISM: Homo sapien
US-10-301-480-91798
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ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 91799
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Patent No. US30020061521A1
APPLICAMT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PCO07
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
Prior application date removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 2442
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 3e-08;
...marches 27; Indels
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; Sequence 83, Application US/10367094
; Publication No. US20040170982A1
; GENERAL INFORMATION:
APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer; FILE REFERENCE: 529452001500
; CURRENT APPLICATION NUMBER: US/10/367,094
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ 1D NOS: 203
; SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.5e-08;
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82.3%;
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Best Local Similarity 86.2%;
Matches 125; Conservative
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US-09-764-869-1276
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Best Local Similarity
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LENGTH: 277616
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Sequence 705208, Application US/10301480

Publication No. US20060057564A1

GENERAL INFORMATION:

TITLE OF INVENTION: Indentifiction and Mapping of Single Nucleotide Polymorphisms

TITLE OF INVENTION: In the Human Genome

FILE REFERENCE: 108827.137

CURRENT FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US/10/301,480

CURRENT FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR RILING DATE: 2001-08-10

PRIOR PILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 705208

LENGTH: 729
RESULT 65
US-10-301-480-705207/c

i Sequence 705207, Application US/10301480

i Publication No. US20060057564A1

i GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: In the Human Genome

TITLE OF INVENTION: In the Human Genome

TITLE OF INVENTION: In the Human Genome

TITLE OF INVENTION: In the Human Genome

TITLE OF INVENTION: In the Human Genome

TITLE OF INVENTION: In the Human Genome

TITLE OF INVENTION: In the Human Genome

CURRENT PELING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR APPLICATION NUMBER: US 60/311,695

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 705207
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Pred. No. 4.2e-09;
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0; Mismatches 27
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14.7%; Score 102.8;
Best Local Similarity 81.5%; Pred. No. 4.28
Matches 119; Conservative 0; Mismatches
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Matches 119; Conservative
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Pred. No. 1.5e-08;
0; Mismatches 19;
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Matches 125; Conservative
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US-10-091-504-1276
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Publication No. US20030059908A1

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFRENCE: PCOOTCI

CURRENT APPLICATION NUMBER: US/10/091,504

CURRENT FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 2442

Prior Application removed - See File Wrapper or Palm

SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: P5018P2
CURRENT APPLICATION NUMBER: US/09/984,429
CURRENT FILING DATE: 2000-110-30
PRIOR APPLICATION NUMBER: 60/244,591
PRIOR APPLICATION NUMBER: 60/244,591
PRIOR PILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-10-09
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Publication No. US20040010132A1
GENERAL INFORMATION:
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Matches 125, Conservative
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ORGANISM: Homo sapiens
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-266-748A-207140

US-10-539-228-366

US-10-539-228-456

US-11-266-748A-60109

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US-11-266-748A-117289
US-11-266-748A-156453
US-11-266-748A-288898
US-11-266-748A-288898
US-11-266-748A-399825
US-11-266-748A-399825
US-10-506-549-3
US-10-506-549-3
US-10-566-748A-20455
US-11-266-748A-20455
US-11-266-748A-20455
US-11-266-748A-20459
US-11-266-748A-20459
US-11-266-748A-20108
US-11-266-748A-25123
US-11-266-748A-25123
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US-11-266-748A-29045
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US-11-266-748A-29045
US-11-266-748A-29045
US-11-266-748A-29045
US-11-266-748A-29045
US-11-266-748A-29045
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US-11-266-748A-200176
US-11-266-748A-60803
US-11-266-748A-211402
US-11-266-748A-211402
US-10-519-335-37
US-11-266-748A-59086
US-11-266-748A-200842
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## ALIGNMENTS

VB-11-266 748A-196825/C

Sequence 196825, Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:
APPLICANT: Harkin, Paul

APPLICANT: Harkin, Paul

TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (139189)

CURRENT APPLICATION WHMBER: US/11/266,748A

CURRENT APPLICATION NUMBER: EP 04105479.2

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR PILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR PILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

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nucleic acids for the improved treatment of breast cell tive disorders
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       49.0%; Pred. No. 3.2e-10;
:ive 0; Mismatches 324;
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CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR EMPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
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; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: ROENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMRICH, Inko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LOOK, Maxime P.
APPLICANT: MARX, Almuth
APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucl
TITLE OF INVENTION: proliferative
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SCHMITT, Manfred
                             Matches 312; Conservative
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         Best Local Similarity
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APPLICANT: FOEKENS, John
APPLICANT: HARBECK, Nadia
APPLICANT: MAIER, Sabine
APPLICANT: MODEL, Fabian
APPLICANT: MODEL, Fabian
APPLICANT: NUMBAICH, Inko
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, And Fed
APPLICANT: SCHMITT, And Fed
APPLICANT: HOEFLER, Heinz
APPLICANT: HOEFLER, Heinz
APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
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                                                                                                                                                                                                                                                                                                                                                            Length 1000;
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Pred. No. 4.9e-11;
0; Mismatches 22;
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CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR FILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-04-17
PRIOR FILING DATE: 2000-01-07
PRIOR PILING DATE: 2000-01-07
PRIOR PILING DATE: 2002-10-01
PRIOR FILING DATE: 2002-10-01
PRIOR FILING DATE: 2002-10-01
PRIOR FILING DATE: 2002-10-01
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PRIOR FILING DATE: 2002-10-01
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
SEQ ID NO 196825
LENGTH: 1000
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Best Local Similarity 84.9%;
Matches 124; Conservative
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                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-196825
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CURRENT APPLICATION NUMBER: US/10/539,228
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR FILING DATE: 2002-12-18
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                SEQ ID NO 214
LENGTH: 72678
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LENGTH: 70665
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                                                                                                                                                                                                                                                           OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                            DB 6; Length 8666;
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APPLICANT: David W. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: CHIR0052-101 (PP023370.0003)
                                                                                                                                                                                                                                                                                                                    y Match 15.2%; Score 106.6; DB 6; Length Local Similarity 49.0%; Pred. No. 3.2e-10; nes 312; Conservative 0; Mismatches 324; Indels
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PRIOR APPLICATION NUMBER: DE 1031/323.v
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR FILING DATE: 2003-01-07
PRIOR PELING DATE: 2002-10-01
PRIOR FILING DATE: 2022-10-01
SEQ ID NO 557
SEQ ID NO 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 214, Application US/10539228; Publication No. US20060154250A1; GENERAL INFORMATION:
                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         12 AAAGTTTTTTTTT
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                                                                                                                                                                                      Gaps
                                                                         Length 72678;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al.
                                                                           Score 104.6; DB 6;
Pred. No. 8.7e-10;
0; Mismatches 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ludwig Institute for Cancer Research TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES FILE REFERENCE: 28967/199178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR PLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: Patentin 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 596, Application US/10505928; Publication No. US20060088532A1; GENERAL INFORMATION:
                                                                         14.9%;
                                                                       Query Match
14.9
Best Local Similarity 80.8
Matches 122; Conservative
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TYPE: DNA ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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2 IGTITCACATAAAGITITITITITITITGAIGATITITAATAAAATAICATITITITITATA
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| Sequence 197923, Application US/11266748A
| Publication No. US20060134663A1
| GENERAL INFORMATION:
| APPLICANT: Harkin, Paul
| APPLICANT: Harkin, Paul
| APPLICANT: Harkin, Paul
| APPLICANT: Harkin, Paul
| APPLICANT: Johnston, Patrick
| TITLE OF INVENTION: Methods of Using the Same
| TITLE OF INVENTION: Methods of Using the Same
| TITLE OF INVENTION: Methods of Using the Same
| TITLE OF INVENTION: Methods of Using the Same
| TITLE OF INVENTION: Methods of USing the Same
| TITLE OF INVENTION: Methods of USing the Same
| TITLE OF INVENTION: Mouber: EP 0410549.2
| PRIOR FILING DATE: 2004-11-03
| PRIOR FILING DATE: 2004-11-03
| PRIOR PILING DATE: 2004-11-03
| PRIOR PAPLICATION NUMBER: EP 04105485.9
| PRIOR PAPLICATION NUMBER: EP 04105486.9
| PRIOR PAPLICATION NUMBER: EP 04105486.9
| PRIOR PELING DATE: 2004-11-03
| PRIOR PELING DATE: 2004-11-03
| PRIOR PELING DATE: 2004-11-03
| PRIOR PELING DATE: 2004-11-03
| PRIOR PELING DATE: 2004-11-03
| PRIOR PELING DATE: 2004-11-03
| PRIOR PELING DATE: 2006-01-18
| PRIOR APPLICATION NUMBER: US 60/662,276
| PRIOR APPLICATION NUMBER: US 60/00,293
| PRIOR PELING DATE: 2005-07-18
| NUMBER: OF SEQ 1D NOS: 483996
| CONTEMBER: OF SEQ 1D NOS: 483996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1000;
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Pred. No. 3.4e-09;
0; Mismatches 21;
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14.3%; Score 99.8; DB 8;
Best Local Similarity 73.1%; Pred. No. 4.1e-09;
Matches 128; Conservative 0; Mismatches 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 TGCTGGTGTGCTGCACCCATTAACTC 161
PRIOR FILING DATE: 2005-03-14
PRIOR PELLANG DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
SEQ ID NO 25751
LENGTH: 1577
                                                                                                                                                                                                                                                          14.3%;
84.9%;
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                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                    ; ORGANISM: Homo Sapiens
US-11-266-748A-25751
                                                                                                                                                                                                                                                                                  Local Similarity
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US-11-266-748A-197923
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ORGANISM:
                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                            Query Match
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              Length 1615;
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APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2006-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
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PRIOR PLING DATE: 2004-11-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 86.1
Matches 124; Conservative
         Mulligan, Karl
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APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Mulligan, Karl
ITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REPERENCE: 55815-0102 (1319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR PILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
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      Methods of Using the Same
      TITLE OF INVENTION: METGOGS OI USING STATES OF UNIVERSITY PRESENCE: 55815-0102 (319189); CURRENT APPLICATION NUMBER: US/11/266,748A; CURRENT FILING DATE: 2005-11-03; PRIOR APPLICATION NUMBER: EP 04105479.2 PRIOR PELING DATE: 2004-11-03; PRIOR PELING DATE: 2004-11-03; PRIOR APPLICATION NUMBER: EP 04105507.0 PRIOR APPLICATION NUMBER: EP 04105507.0 PRIOR APPLICATION NUMBER: EP 04105507.0 PRIOR APPLICATION NUMBER: EP 04105507.0 PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-18
PRIOR PILING DATE: 2005-03-18
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PRIOR PILING DATE: 2005-03-18
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PRIOR PILING DATE: 2005-03-18
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APPLICANT: Harkin, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 81.9%;
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-11-266-748A-29041
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APPLICANT: SCHMITT, Manfred
APPLICANT: SCHMITT, Manfred
APPLICANT: SCHMITT, Manfred
APPLICANT: SCHMITT, Maxime P.
APPLICANT: LOOK, Maxime P.
APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
TITLE OF INVENTION: Momber: 2004-12-11
PRIOR APPLICATION NUMBER: US/10/517,441
CURRENT APPLICATION NUMBER: US/10/517,441
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR FILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-04-17
PRIOR PRILING DATE: 2003-01-07
PRIOR PLILING DATE: 2003-01-07
PRIOR PLILING DATE: 2003-01-07
PRIOR PLILING DATE: 2003-01-07
PRIOR PLILING DATE: 2003-01-07
PRIOR PLILING DATE: 2002-10-01
SPRIOR PLILING DATE: 2002-10-01
SPRIOR PLILING DATE: 2002-10-01
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541 GTATACATGTGCCATGTGTGTGTGCTGCACCCATTAACTCGCTAAAGTCTGTTTT 595
                                                                                                                             122 ATATACATGTGCCATGCTGCTGCACCCATTAACTCACATGAAGTTTTTT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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5e-09;
thes 32; Indels 0
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Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
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Pred. No. 5e-09
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 Sequence 19, Application US/10517441 Publication No. US20060121467A1 GENERAL INFORMATION:
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78.8%;
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APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: MAIER, Sabine
APPLICANT: MARTENS, John
APPLICANT: MODEL, Fabian
APPLICANT: NIMMRICH, Inko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo Sapiens
US-10-517-441-19
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20766 AATGIGCAGGITAGITACATATGIATACAIGTGCCATGCTGGTGTGCTGCACCCATTAAC 20707
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40 AAAATATCATTTTTTTTTTTATTATTATTATTAAGTTTTTAGGGTACATGTGCAA
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                                                                                                                                                                                          RESULT 13
US-10-539-228-826/c
| Sequence 826, Application US/1053928
| Sequence 826, Application US/1053928
| Publication No. US20060154250A1
| GENERAL INFORMATION:
| APPLICANT: David W. Morris
| APPLICANT: Marc S. Malandro
| TITLE OF INVENTION: Novel Compositions and Methods in Cancer FILE REFERENCE: CHRO052-101 (PP023370.003)
| CURRENT APPLICATION NUMBER: US/10/539,228
| CURRENT FILING DATE: 2005-06-17
| PRIOR APPLICATION NUMBER: US 10/322,281
| PRIOR PILING DATE: 2002-12-18
| NUMBER OF SEQ ID NOS: 866
| SOFTWARE: FeatSEQ for Windows Version 4.0
| SEQ ID NO 826
| LIENGTH: 83965
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US-11-266-748A-61303

SQUENCE 61303, Application US/11266748A

SQUENCE 61303, Application US/11266748A

SQUENCE 61303, Application US/11266748A

SQUENCE 61303, Application US/11266748A

SQUENCE 61303, Patrick

APPLICANT: Muligan, Rarl

TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: TRANSCRIPTOME Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)

FILE REFERENCE: 55815-0102 (319189)

FILE REFERENCE: 55815-0102 (319189)

FRIOR APPLICATION NUMBER: EP 04105479.2

SPRIOR APPLICATION NUMBER: EP 04105482.6

SPRIOR PELLING DATE: 2004-11-03

SPRIOR FILING DATE: 2004-11-03

SPRIOR PILING DATE: 2004-11-03

SPRIOR PELLING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105507.0

SPRIOR APPLICATION NUMBER: EP 04105485.9

SPRIOR APPLICATION NUMBER: EP 04105485.9

SPRIOR APPLICATION NUMBER: EP 04105484.2
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Pred. No. 9.1e-09;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , LUCATION: (1)...(83965); OTHER INFORMATION: n = A,T,C or G US-10-539-228-826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                  Score 99.6; DB 8; Length 122568; Pred. No. 6.8e-09; 0; Mismatches 29; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hartin, Paul
APPLICANT: Hartin, Paul
APPLICANT: Hartin, Paul
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 5815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 0410548.6
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-01-03
PRIOR FILING DATE: 2005-01-04
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6962 ATACATGTGCCACGCTGCTGCACCACTAACTC 6999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 ATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 205304, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 23292
LENGTH: 122568
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 81.0%;
Matches 128; Conservative
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Best Local Similarity 76.28
Matches 122; Conservative
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US-11-266-748A-205304
                                                                                                                                         TYPE: DNA
ORGANISM: Homo Sapiens
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US-11-266-748A-205304
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Sequence 456, Application US/10539228

Publication No. US2006015425041

GENERAL INFORMATION:

APPLICANT: David W Morris

APPLICANT: David W Morris

APPLICANT: David W Morris

TILE OF INVENTON: Novel Compositions and Methods in Cancer

FILE REFERENCE: CHIROS2-101 (PP023370.0003)

CURRENT APPLICATION NUMBER: US/10/539,228

CURRENT APPLICATION NUMBER: US/10/339,228

FILE REPERENCE: CHIROS2-101 (PP023370.0003)

CURRENT APPLICATION NUMBER: US/10/332,281

PRIOR APPLICATION NUMBER: US 10/322,281

PRIOR FILING DATE: 2005-10-18

NUMBER OF SEQ ID NOS: 866

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 456

LENGTH AD 177
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Publication No. US20060154250A1

GENERAL INPORMATION:
APPLICANT: David W. Morris

TITLE OF INVENTION: Novel Compositions and Methods in Cancer;
FILE REFERENCE: CHR0052-101 (PP023370.0003)

CURRENT APPLICATION NUMBER: US/10/539,228

CURRENT FILING DATE: 2005-06-17

PRIOR APPLICATION NUMBER: US 10/322,281

PRIOR PELLING DATE: 2002-12-18

NUMBER OF SEQ ID NOS: 866

SOFTWARE: RestSEQ for Windows Version 4.0
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                                                                                                                                        137 GCTGGTGTGCTGCACCCATTAACTC 161
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NAME/KEY: misc feature

LOCATION: (1)...(301477)

OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                        US-10-539-228-456/c
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LENGTH: 52987
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                                                                                                                                                                                                                                                                                                                                      22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REPREBLOE: 55815-0102 (319189)
CURRENT APPLICAN UNMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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84.2%; Pred. No. 9.4e-09;
iive 0; Mismatches 22;
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Best Local Similarity 84.1%; Pred. No. 9.2e-09;
Matches 122; Conservative 0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104954 TGTTGGTGTGCTGCACCCATTAACTC 104979
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PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-01-03
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PALENTIN VERSION 3.3
SEQ ID NO 207140
TYPE: DAA
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PATEHTIN VERSION 3.3
SEQ ID NO 61303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 TGCTGGTGTGCTGCACCCATTAACTC 161
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                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 84.24
Matches 123; Conservative
                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-61303
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US-11-266-748A-207140
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US-11-266-748A-207140
                                                                                                                                                                               LENGTH: 110096
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28779 -TAAGTTTTAGGTACATGTGCACATTGTGCAGGTTAGTTACATATGTATACATGTGCCA 28721
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                                                        1; Gaps
Score 97.4; DB 6; Length 52987; Pred. No. 1.5e-08; 0; Mismatches 21; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
ITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REPERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105492.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-01-18
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCATGTTGGTGTGCTGCACCCGTTAACTC 346
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                                                                                                                                                                                                                                                                                                                                             28720 TGCTGGTGCGCTGCACCACTAA 28698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 209478, Application US/11266748A; Publication No. US20060134663A1; GENERAL INFORMATION: APPLICANT: Harkin, Paul
                                                                                                                                                                                                                                                                                                               TGCTGGTGTGCTGCACCCATTAA 158
Query Match
Best Local Similarity 84.6%;
Matches 121; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 78.0
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo Sapiens
US-11-266-748A-209478
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US-11-266-748A-209478/c
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RESULT 19

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US-11-266-748A-60109
Sequence 60109, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Mulligan, Kari
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
CURRENT FILING DATE: 2005-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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PRIOR PELING DATE: 2004-11-03
                                                                                   APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: GIRIO052-101 (PPC23370,0003)
CURRENT APPLICATION NUMBER: US/10/539,228
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: US 10/322,281
RAING DATE: 2002-12-18
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FASTSEQ for Windows Version 4.0
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2e-08;
thes 38; Indels
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Pred. No. 2e-0
0; Mismatches
Sequence 456, Application US/10539228
Publication No. US20060154250A1
GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-10-539-228-456
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Best Local Similarity 75.9%;
Matches 120; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
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                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 456
LENGTH: 301477
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APPLICANT: Vance, Jeffrey M.
APPLICANT: Vance, Jeffrey M.
APPLICANT: Kraus, William E.
APPLICANT: Goldschmidt, Pascal J.
APPLICANT: Goldschmidt, Pascal J.
APPLICANT: Gregory, Simon G.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING GENETIC MARKERS WITH
TITLE OF INVENTION: CARDIOVASCULAR DISEASE
FILE REPERENCE: 5405-347
CURRENT APPLICATION NUMBER: US/11/260,842
CURRENT FILING DATE: 2005-10-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            499
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WESULT 226

WESULT 226

WESULT 226

WEDLICART 341545/C

WEDLICART 100 US20060134663A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Harkin, Paul

APPLICANT: Harkin, Paul

TITLE OF INVENTION: Rethods of Using the Same

FILE REFERENCE: 55815-0102 (119189)

CURRENT APPLICATION: Methods of Using the Same

FILE REFERENCE: 55815-0102 (1319189)

CURRENT APPLICATION WOMBER: US/11/266,748A

CURRENT PLING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR PLING DATE: 2004-11-03

PRIOR PLING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR APPLICATION NUMBER: US 60/700,293

PRIOR PLING DATE: 2004-11-03

PRIOR PLING DATE: 2005-03-14

PRIOR FILING DATE: 2005-03-14

PRIOR PLING DATE: 2005-03-14

PRIOR PLING DATE: 2005-03-14

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Pred. No. 1.4e-08;
0; Mismatches 32; Indels 1
        562 GTATACATGTGCCATATTGGTGTGCTGCACCCATTAACTC 601
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PRIOR FILING DATE: 2004-10-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 79.4%;
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo Sapiens
US-11-266-748A-341545
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APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2004-11-03
PRIOR PAPLICATION NUMBER: EP 04105492.6
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
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                                                                                                                                                                                          Score 97; DB 8; Length 131546; Pred. No. 2e-08;
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                                                                                                                                                                                                                                                                   40; Indels
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Pred. No. 1.4e-08;
0; Mismatches 32;
                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 290116, Application US/11266748A Publication No. US20060134663A1
                                                                                                                                                                                      13.9%;
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Best Local Similarity 79.4%;
Matches 127; Conservative
                                                                                                                                                                              Query Match
Best Local Similarity 75.21
Matches 121; Conservative
                                    ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-60109
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US-11-266-748A-290116
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Best Local Similarity
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LENGTH: 131546
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US-11-266-748A-117289/c
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                                                                                                                                                                              Length 261789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
                                                                                                                                                                                                                          Indels
                                                                                                                                                                              Query Match
13.8%; Score 96.8; DB 8;
Best Local Similarity 84.0%; Pred. No. 2.3e-08;
Matches 121; Conservative 0; Mismatches 22;
                                                                                                                                                                                                                                                                      17 TTTTTTTTTTGATGATTTTAATAAAATATCATTTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TILLE REFERENCE: 5815-0102 (31918)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT APPLICATION NUMBER: US/11/266,748A
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR SEQ ID NOS: 488996
NUMBER OF SEQ ID NOS: 488996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             257606 GCGGGTGCGCTGCACTAACT 257583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-11-266-748A-28210/c; Sequence 28210, Application US/11266748A; Publication No. US20060134663A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTGGTGTGCTGCACCCATTAACT 160
                  SOFTWARE: Patentin version 3.3
SEQ ID NO 1
LENGTH: 261789
NUMBER OF SEQ ID NOS: 39
                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-260-842-1
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US-11-266-748A-28210
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LENGTH: 421987
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APPLICANT: Johnston, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Minitigan, Karl
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
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TITLE OF INVENTION: Methods of Using the Same
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PLING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
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US-11-266-748A-159453
is Sequence 159453, Application US/11266748A
; publication No. US20060134663A1
; GENERAL INPORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Harkin, Paul
; APPLICANT: Willigan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same
; FILE REPRENCE: 55815-0102 (119189)
; CURRENT APPLICATION UNMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 TGCTGGTGTGCTGCACCCATTAACTC 161
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                                                48674 recresificacióciócaccaciase 48651
                                                                                                                                                                                                          Sequence 117289, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
136 TGCTGGTGTGCTGCACCCATTAAC 159
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 117289
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Best Local Similarity 78.8<sup>†</sup>
Matches 115; Conservative
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CORGANISM: Homo Sapiens
US-11-266-748A-117289
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926 TIAAGTITTAGGGTACATGTGCACAACGTGCAGGTTTGTTACATATGTAACATGTGCCA 867
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                                                                                                                                                                                                         Query Match 13.8%; Score 96.4; DB 8; Length 1000; Best Local Similarity 78.8%; Pred. No. 1.6e-08; Matches 115; Conservative 0; Mismatches 31; Indels 0.
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78.8%;
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Best Local Similarity 78.8
Matches 115; Conservative
                                           TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-288898
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US-11-266-748A-340327
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                   LENGTH: 1000
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APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 5815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
FRIOR APPLICATION NUMBER: EP 04105482.6
FRIOR FILING DATE: 2004-11-03
FRIOR APPLICATION NUMBER: EP 04105483.4
FRIOR APPLICATION NUMBER: EP 04105483.4
FRIOR APPLICATION NUMBER: EP 04105483.9
FRIOR FILING DATE: 2004-11-03
FRIOR PELING DATE: 2004-11-03
FRIOR PELING DATE: 2004-11-03
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FRIOR FILING DATE: 2005-03-14
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Pred. No. 1.6e-08;
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PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PELLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PAPLICATION NUMBER: EP 04105484.2
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
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PRIOR FILING DATE: 2005-07-18
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Publication No. US20066134663A1
GENERAL INFORMATION:
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Best Local Similarity 78.8%;
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; ORGANISM: Homo Sapiens
US-11-266-748A-159453
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STATEMENT IN FORMATION:

APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
ITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE OF INVENTION: WHORER: US/11/266,748A
CURRENT FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PAPLICATION NUMBER: EP 04105482.9
PRIOR PILING DATE: 2004-11-03
PRIOR PAPLICATION NUMBER: EP 04105485.9
PRIOR PILING DATE: 2004-11-03
PRIOR PAPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
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Pred. No. 1.6e-08;
0; Mismatches 31;
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0; Mismatches
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NOS 483996
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SOFTWARE: FastSEQ for Windows Version 4.0
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LOCATION: (1)...(394191)

OTHER INFORMATION: n = A,T,C or G

US-10-506-549-3
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Best Local Similarity 78.8%;
Matches 115; Conservative
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Best Local Similarity 78.8°
Matches 115; Conservative
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US-11-266-748A-470871
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ORGANISM: Homo sapiens
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LENGTH: 394191
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APPLICANT: HOUSENIN, PARTICK
APPLICANT: Mulligan, Karl
ITILE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT PILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PELLING DATE: 2004-11-03
PRIOR PELLING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PELLING DATE: 2005-01-03
PRIOR FILING DATE: 2005-01-03
PRIOR FILING DATE: 2005-01-18
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PRIOR FILING DATE: 2005-01-18
PRIOR FILING DATE: 2005-01-18
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; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Methods of Using the Same
; TITLE OF INVENTION: Methods of Using the Same
; TITLE OF INVENTION: Methods of Using the Same
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR FILING DATE: 2004-11-03
; PRIOR PLILING UNTER: EP 04105479.2
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13.8%; Score 96.4; DB 8;
Best Local Similarity 78.8%; Pred. No. 1.6e-08;
Matches 115; Conservative 0; Mismatches 31;
              135 TGGTGGTGTGCTGCACCCATTAACTC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 TGCTGGTGTGCTGCACCCATTAACTC 161
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                                                                                                                                                  Sequence 399825, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
APPLICANT: Harkin, Paul
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US-11-266-748A-399825
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Sequence 3, Application US/10506549
Publication No. US20060100417A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: APPLERA CORPORATION
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: CLOO1361-US
CURRENT APPLICATION NUMBER: US/10/506,549
CURRENT FILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: 60/361,343
PRIOR FILING DATE: 2002-03-05
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                                                         Gaps
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     Length 1000;
Score 96.4; DB 8; Length 1
Pred. No. 1.6e-08;
0; Mismatches 31; Indels
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1; Gaps

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629225 TAAGTITTAGGGTACATGTGCACAATGTGCAGGTTAGTTACATATGTATACATGTGCCAT 629166
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US-11-266-748A-25123/C

Sequence 25123, Application US/11266748A

Sequence 25123, Application US/11266748A

Publication No. US20060134663AI

GENERAL INFORMATION:

APPLICANT: Hartin, Paul

TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (1319189)

CURRENT APPLICATION UNMERR: US/11/266,748A

CURRENT APPLICATION NUMBER: EP 04105479.2

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR PRIOR PRILOR NUMBER: EP 04105485.9

PRIOR PRILOR DATE: 2004-11-03

PRIOR PRILOR DATE: 2004-11-03

PRIOR PRILOR DATE: 2004-11-03

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PRIOR PRILOR DATE: 2004-11-03

PRIOR PRILOR DATE: 2004-11-03

PRIOR PRILOR DATE: 2004-11-03

PRIOR PRILOR DATE: 2004-01-10

PRIOR FILING DATE: 2005-03-14

PRIOR FILING DATE: 2005-03-14

PRIOR FILING DATE: 2005-03-14

PRIOR PILING DATE: 2005-03-14

PRIOR PILING DATE: 2005-03-14

PRIOR PILING DATE: 2005-03-14

PRIOR PILING DATE: 2005-03-14
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   PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE. 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 29045
LENGTH: 755217
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Best Local Similarity 83.4%;
Matches 121; Conservative
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Best Local Similarity 78.2'
Matches 115; Conservative
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ORGANISM: Homo Sapiens
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ORGANISM: Homo Sapiens
US-11-266-748A-25123
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54974 TGTGCACAATGTGCAGGTTAGTTACATATGTATACATGTGCCATGCTGGTGTGCTGCACC 54915
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Pred. No. 2.7e-08;
0; Mismatches 13; Indels 1;
                                                                                                                                                                                                                                                                                            Sequence 232, Application US/1053928
| Publication No. US20060154250A1
| GENERAL INPORMATION:
| APPLICANT: David W. Morris
| APPLICANT: Marc S. Malandro
| TITLE OF INVENTION: Novel Compositions and Methods in Cancer
| FILE REFERENCE: CHIR0052-101 (PP023370.0003)
| CURRENT APPLICATION NUMBER: US/10/539,228
| CURRENT APPLICATION NUMBER: US/10/539,228
| PRIOR APPLICATION NUMBER: US/10/322,281
| PRIOR APPLICATION NUMBER: US/10/322,281
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| PRIOR APPLICATION NUMBER: US/10/322,281
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| PRIOR APPLICATION NUMBER: US/10/322,281
| PRIOR APPLICATION NUMBER: US/10/322,281
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APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
CURRENT APPLICATION WUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION WUMBER: EP 04105483.4
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION WUMBER: EP 04105485.9
                                                                                                                           137068 TACTGGTGTGCTGCACCCATTAACTC 137093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (1)...(135827)
; OTHER INFORMATION: n = A,T,C or G
US-10-539-228-232
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Best Local Similarity 89.1%;
Matches 115; Conservative (
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US-10-539-228-232/c
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APPLICANT: Mulligan, Karl
APPLICANT: Mulligan, Karl
APPLICANT: Mulligan, Karl
APPLICANT: Mulligan, Karl
TITLE OF INVENITON: Transcriptome Microarray Technology and
TITLE OF INVENITON: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2006-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
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13.7%; Score 95.6; DB 8; Length 1000;
Best Local Similarity 82.4%; Pred. No. 2.2e-08;
Matches 122; Conservative 0; Mismatches 24; Indels 2
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; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
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US-11.266-748A-204505
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US-11-266-748A-204505/c
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TITLE OF INWENTOR. Transcriptone Microarray Technology and TITLE OF INWENTOR. Transcriptone Microarray Technology and TITLE REPRENEE: 58915-010 (13198)

CURRENT FILING DATE: 2009-11-03

FRICK PALLOATION NUMBER: DE 0410549.2

FRICK PALLOATION NUMBER: DE 0410549.2

FRICK PALLOATION NUMBER: DE 0410549.2

FRICK PALLOATION NUMBER: DE 0410549.3

FRICK PALLOATION NUMBER: DE 0410549.3

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Sequence 335897, Application US/11266748A

Publication No. US20660134663A1

GENERAL INFORMATION:
APPLICANT: Harkin, Paul

TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 58815-0102 (139189)

CURRENT APPLICATION NUMBER: US/11/266,748A

FILE REPERENCE: 5805-011-03

FRIOR PILING DATE: 2004-11-03

FRIOR FILING DATE: 2004-11-03

FRIOR FILING DATE: 2004-11-03

FRIOR PELICATION NUMBER: EP 04105483.4

FRIOR PELING DATE: 2004-11-03

FRIOR APPLICATION NUMBER: EP 04105483.4

FRIOR PELING DATE: 2004-11-03

FRIOR APPLICATION NUMBER: EP 04105484.2

FRIOR PELING DATE: 2004-11-03

FRIOR PELING DATE: 2004-11-03

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FRIOR PELING DATE: 2004-11-03

FRIOR PELING DATE: 2005-07-18

FRIOR PELING DATE: 2005-03-14

FRIOR PELING DATE: 2005-07-18

FRIOR PELING DATE: 2005-07-18

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Publication No. US20060134663A1
GENERAL INFORMATION
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
ITILE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 13.6%; Score 95.2; DB 8; Length 1 Best Local Similarity 82.9%; Pred. No. 2.6e-08; Matches 121; Conservative 0; Mismatches 23; Indels
                                                                                                                                                      585 TGCTGGTGTGCTGCACCCATTAACTC 610
                                                                                                                      136 TGCTGGTGTGCTGCACCCATTAACTC 161
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; ORGANISM: Homo Sapiens
US-11-266-748A-335897
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US-11-266-748A-394477
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APPLICANT: Muligan, Karl
ITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105492.6
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2005-01-14
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PILING DATE: 2005-07-18
                                                                                                                                                                                                                                                                                                               Length 1000;
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13.6%; Score 95.2; DB 8;
Best Local Similarity 82.9%; Pred. No. 2.6e-08;
Matches 121; Conservative 0; Mismatches 23;
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Publication No. US20060134663A1
GENERAL INFORMATION:
PRIOR FILING DATE: 2005-03-14
PRIOR PELIANG NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PALENTIN VERSION 3.3
SEQ ID NO 220785
LENGTH: 1000
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Best Local Similarity 82.9
Matches 121; Conservative
                                                                                                                                                                                                                     ; ORGANISM: Homo Sapiens
US-11-266-748A-220785
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SEQ ID NO 284468
                                                                                                                                                                                              TYPE: DNA
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NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
SEQ ID NO 465523
LENGTH: 1000
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LOCATION: (18413) .. (18436)
OTHER INFORMATION: n is a,
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(19594)..(19695)
                                                                                    TYPE: DNA; ORGANISM: Homo Sapiens
US-11-266-748A-465523
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                                                                                                                                                                           Query Match
Best Local Similarity
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LENGTH: 22884
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NAME/KEY:
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13.6%; Score 95.2; DB 8; Length 1000;
Best Local Similarity 82.9%; Pred. No. 2.6e-08;
Matches 121; Conservative 0; Mismatches 23; Indels 2
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Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: 119189)
CURRENT APPLICATION NUMBER: US/11/266,748A
    FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105492.2

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2005-01-14

PRIOR FILING DATE: 2005-01-14

PRIOR FILING DATE: 2005-01-18

NUMBER OF SEQ ID NOS: 483996

SEC ID NO 394477

LENGTHER: DATE: 2005-07-18

NUMBER OF SEQ ID NOS: 483996

SEC ID NO 394477
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RIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PLILING DATE: 2004-11-03
PRIOR PLILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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APPLICATION NUMBER: US 60/700,293
FILING DATE: 2005-07-18
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US-11-266-748A-394477
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RESULT 42
US-11-347-766-75/C
US-11-347-766-75/C
; Sequence 75, Application US/11347766
; Publication No. US20060134751A1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F
; APPLICANT: Liang, Yinghua
; TITLE OF INVENTION: Identification of Novel Gene Family Members Expressed by
; TILE OF INVENTION: Hematopoietic Cells
; FILE REFERENCE: 180/122 PCT/US
; CURRENT APPLICATION NUMBER: US/11/347,766
; CURRENT FILING DATE: 2006-02-02
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 81
; SOFFWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEXY: genomic_DNA
NACATION: (1). (22884)
OTHER INFORMATION: n is an undetermined nucleotide (dATP, dCTP, dGTP, or dTTP)
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                                                                                         Gaps
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  Length 1000;
13.6%; Score 95.2; DB 8; Length 10
82.9%; Pred. No. 2.6e-08;
tive 0; Mismatches 23; Indels
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LOCATION: (9562)..(9621)
OTHER INFORMATION: n is a, c, g,
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Sequence 219620. Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION.
GENERAL INFORMATION.
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICANT NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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                                                                                             Length 22884;
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APPLICANT: Muligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REPERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
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PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
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                                                                                             13.6%; Score 95.2; DB 8;
83.3%; Pred. No. 3.5e-08;
ative 0; Mismatches 23;
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                                                                                        Query Match
Best Local Similarity 83.3<sup>3</sup>
Matches 120; Conservative
; NAME/KEY: coding region
; LOCATION: (20223)..(20249)
US-11-347-766-75
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Best Local Similarity
Matches 120; Conserv
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SEQ ID NO 25150
LENGTH: 170869
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44 TATCATTTTCTTTTTTATTATTATTATTATTTAAGTTTTTAGGGTACATGTGCAAAGTG 103
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USSULTIATES THEAPENDURE

SEQUENCE (9108, Application US/11266748A

Publication No. US20060134663A1

SEQUENCE INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Mulligan, Karl

TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: WHERE: US011/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

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PRIOR PILING DATE: 2005-03-14

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Pred. No. 2.7e-08;
0; Mismatches 60; Indels
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Best Local Similarity 70.0°
Matches 142; Conservative
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ORGANISM: Homo Sapiens
US-11-266-748A-60108
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104 TGCAGGTTAGTTACATATATATACATGTGCCATGCTGTGTGCTGCACCCATTAACTCAC 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379 AGAATAAGACATGGGGATCTTTTGGGGTGCCATTATTCTCCCTACCACAGTATATTAAGAA 320
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APPLICANT: Harkin, Paul
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PELIOR OFFE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
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13.6%; Score 95; DB 8; Length 81085;
Best Local Similarity 81.9%; Pred. No. 4.2e-08;
Matches 122; Conservative 0; Mismatches 25; Indels
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13.6%; Score 95; DB 8;
Best Local Similarity 70.0%; Pred. No. 2.7e-08;
Matches 142; Conservative 0; Mismatcher
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   PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
SEQ ID NO 239532
LENGTH: 498
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SOFTWARE: PatentIn version 3.3
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US-11-266-748A-25123
                                                                                                                                                                                        ; ORGANISM: Homo Sapiens
US-11-266-748A-239532
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LENGTH: 81085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 TGCAGGTTAGTTACATATATATACTGCCATGCTGGTGTGCTGCACCACTAACTCAC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 ATGAAGTTTTTTTAAATTTTAGTGACAGTTTTTAGTCATTTTCCTAATTGAAAGTATCAT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 AGAATAAGACATGGGGATCTTTGGGGTGCCATTATTCTCCCTACCACAGTATTAAGAA 179
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Sequence 229532, Application US/11266748A

Publication No. US2060134663A1

SEGNERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Johnston, Patrick

APPLICANT: Mulligan, Kari

TITLE OF INVENTION: Methods of Using the Same

TITLE OF INVENTION: Methods of Using the Same

TITLE OF INVENTION: Methods of Using the Same

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

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PRIOR PELING DATE: 2004-11-03

PRIOR PELING DATE: 2006-03-14

PRIOR PELING DATE: 2005-03-14

PRIOR PELING DATE: 2005-03-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DÀTE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-03-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 70.0 Matches 142, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo Sapiens
US-11-266-748A-219620
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TANGO129 AND INTEGRIN ALPHA SUBUNIT PROTEIN
11 TAAAGITITITITITITIGAIGATITITAATAAATATCATITITITITITITATTA 70
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TITLE OF INVENTION: DELTA3, USER
TITLE OF INVENTION: SPOIL, NEOKINE, TANGO129 AND INTEGRIN ALPHA SUBUNIT
TITLE OF INVENTION: ADD NUCLEIC ACID MOLECULES AND USES THEREOF
FILE REFERENCE: MP105-0100MNIN
CURRENT APPLICATION NUMBER: US/11/175,714
CURRENT TILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 09/868,218
PRIOR FILING DATE: 2000-05-09
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1997-06-11
PRIOR PRIOR APPLICATION NUMBER: US 09/832,633
PRIOR FILING DATE: 1997-04-04
PRIOR FILING DATE: 1997-04-04
PRIOR FILING DATE: 2004-07-21
PRIOR PRIOR PRIOR FILING DATE: 2001-05-22
PRIOR FILING DATE: 2001-05-22
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Pred. No. 4.5e-08;
0; Mismatches 35; Indels 0
                                                                                                                                  135685 CGCCATGCTGGTGCTGCACCCACTAACTC 135715
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                           Sequence 87, Application US/11175714 Publication No. US20060122373A1 GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-11-175-714-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan, Yang
Busfield, Samantha J.
                                                                                                                                                                                                                                                                                                                                                                                                                                       McCarthy, Sean A.
Gearing, David
Holtzman, Douglas A.
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76.8%;
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Mackay, Charles
Lora, Jose M.
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Matches 116; Conservative
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ORGANISM: Homo Sapiens
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NAME/KEY: misc_feature
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APPLICANT:
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APPLICANT: Barnes, Thomas M.
APPLICANT: Barnes, Thomas M.
APPLICANT: Barnes, Thomas M.
TITLE OF INVENTION: DELTA3, FTHMA-070, TANGOBS, TANGOT7,
TITLE OF INVENTION: SPDIL, NEGKINE, TANGOL29 AND INFEGRIN ALPHA SUBUNIT PROTEIN
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES AND USES THEREOF
FILE REFERENCE: MPIOS-0100MNIM CACID MOLECULES AND USES THEREOF
GURRENT FILING DATE: 2005-07-05
FRICK PPLICATION NUMBER: US 10/417,719
FRIOR APPLICATION NUMBER: US 10/917,719
FRIOR APPLICATION NUMBER: US 09/568,218
FRIOR APPLICATION NUMBER: US 09/912,855
FRIOR PLING DATE: 1997-06-11
FRIOR APPLICATION NUMBER: US 10/105,934
FRIOR PLING DATE: 2004-07-21
FRIOR APPLICATION NUMBER: US 10/105,934
FRIOR PLING DATE: 2004-07-21
FRIOR APPLICATION NUMBER: US 09/062,389
FRIOR APPLICATION NUMBER: US 09/062,389
FRIOR APPLICATION NUMBER: US 09/062,389
FRIOR APPLICATION NUMBER: US 09/062,017
FRIOR APPLICATION NUMBER: US 09/062,017
FRIOR APPLICATION NUMBER: US 09/062,017
FRIOR APPLICATION NUMBER: US 09/062,017
FRIOR PLING DATE: 1997-04-18
FRIOR APPLICATION NUMBER: US 09/062,017
FRIOR FILING DATE: 1997-04-18
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                                                             Gaps
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                                                                                                                                                                                                                   19058 CCATGCTGGTGCGCTGCACCACTAACTC 19086
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                                                                                                                                                                                   CCATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Millennium Pharmaceuticals, Inc. APPLICANT: McCarthy, Sean A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 86 LENGTH: 152331
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 86, Application US/11175714
Publication No. US20060122373A1
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OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McCarthy, Sean A.
Gearing, David
Holtzman, Douglas A.
Pan, Yang
Busfield, Samantha J.
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LOCATION: (1)...(15233
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71 TACTITITAAGITITIAGGGTACATGTGCAAAGTGTGCAGGTTAGTTACATATATACATG 130
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.DCATION: (448538)..(448538)

. OTHER INFORMATION: n is a, c, g, or t

US-11-266-748A-28223
                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (202671)..(202672)
OTHER INFORMATION: n is a, c,
                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (202680)..(202680)
OTHER INFORMATION: n is a, c,
NAME/KEY: misc feature
LOCATION: (202648)..(202648)
OTHER INFORMATION: n is a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (202691)..(202691)
OTHER INFORMATION: n is a, c,
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NAME/KEY: misc_feature
LCCATION: (202701)..(202702)
OTHER INFORMATION: n is a, c,
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LOCATION: (202712)..(202714)
OTHER INFORMATION: n is a, c,
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LOCATION: (448497)..(448497)
OTHER INFORMATION: n is a, c,
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NAME/KEY: misc_feature
LOCATION: (202684)
OTHER INFORMATION: n is a, c,
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LOCATION: (202586)..(202686)
OTHER INFORMATION: n is a, c,
FEATURE:
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LOCATION: (202696)..(202697)
OTHER INFORMATION: n is a, c,
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LOCATION: (448499)..(448500)
OTHER INFORMATION: n is a, c,
                                                                                          NAME/KEY: misc feature
LOCATION: (202661)..(202661)
OTHER INFORMATION: n is a, c,
                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: (202663)
OTHER INFORMATION: n is a, c,
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Best Local Similarity 76.8<sup>1</sup>
Matches 116; Conservative
                                                                                                                                                                                                                                                         FEATURE:
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                                                                                                               RESULT 50

US-11-266-748A-28223

Sequence 28223, Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Johnston, Patrick

APPLICANT: Johnston, Patrick

TITLE OF INVENTION: Transcriptome Microarray Technology and

TITLE OF INVENTION: Transcriptome Microarray Technology and

FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A
  PRIOR PELICATION NUMBER: EP 04105479.2
PRIOR PELICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105507.0
PRIOR PELICATION NUMBER: EP 04105507.0
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/602,276
PRIOR PELING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
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LOCATION: (42263)..(42263)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
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LOCATION: (42256)..(42256)
OTHER INFORMATION: n is a, c, g,
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NAME/KEY: misc_feature
LOCATION: (42260) ..(42260)
OTHER INFORMATION: n is a, c,
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LOCATION: (14173)..(14173)
OTHER INFORMATION: n is a, c,
FEATURE:
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LOCATION: (205\(\bar{a}\)2. (206\(\bar{a}\)1)
OTHER INFORMATION: n is a, c,
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NAME/KEY: misc_feature
LOCATION: (14162)..(14163)
OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (21980)..(21980)
OTHER INFORMATION: n is a,
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LOCATION: (21992)..(21992)
OTHER INFORMATION: n is a,
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ORGANISM: Homo Sapiens
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LENGTH: 495475
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Query Match 13.5%; Score 94.8; DB 8; Length 104644; Best Local Similarity 78.1%; Pred. No. 4.7e-08; Matches 114; Conservative 0; Mismatches 32; Indels 0;
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| FEATURE:
| NAME/KEY: MS4A12 coding_region
| LOCATION: (101182)..(101283)
| FEATURE:
| NAME/KEY: misc_feature
| LOCATION: (104561)..(104625)
| OTHER INFORMATION: n is a, c, g, or t
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US-11-266-748A-29045
; Sequence 29045, Application US/11266748A
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                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (32640)..(32640)
OTHER INFORMATION: n is a, c, g, or t
                                                                                                                                                                                                                                                             MS4A5 initial coding_region (64028)..(64180)
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                                  MS4A7 coding region (23741)..(23947)
                                                                                    NAME/KEY: MS4A7 coding region
LOCATION: (27037)..(27138)
                                                                                                                                     NAME/KEY: MS4A7 coding region LOCATION: (28139)..(28210)
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(65149)..(65277)
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(82002)..(82109)
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LOCATION: (21068)..(21124)
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LOCATION:
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                                     NAME/KEY:
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LOCATION: (1)..(104644)
OTHER INFORMATION: n is an undetermined nucleotide (dATP, dCTP, dGTP, or dTTP)
                                                                                              APPLICANT: Tedder, Thomas F
APPLICANT: Tedder, Thomas F
APPLICANT: Liang, Yinghua
TITLE OF INVENTION: Identification of Novel Gene Family Members Expressed by
TITLE OF INVENTION: Hematopoietic Cells
FILE REFERENCE: 180/132 PCT/US
CURRENT APPLICATION NUMBER: US/11/347,766
CURRENT FILING DATE: 2006-02-02
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn version 3.2
SEQ ID NO 79
LENGTH: 104644
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NAME/KEY: misc feature
LOCATION: (11699)..(11699)
OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: MS4A7_initial_coding_region
LOCATION: (17493)..(17639)
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                              US-11-347-766-79/c
; Sequence 79, Application US/11347766
; Publication No. US20060134751A1
; GENERAL INFORMATION:
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LOCATION: (143)..(143)
OTHER INFORMATION: n is a, c,
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LOCATION: (19439)..(19573)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)._(3)
OTHER INFORMATION: n is a, c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (39)...(39)
OTHER INFORMATION: n is a, c
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NAME/KEY: misc_feature
LOCATION: (73)...(73)
OTHER INFORMATION: n is a,
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LOCATION: (362). (362)
OTHER INFORMATION: n is a,
FEATURE:
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LOCATION: (11659)..(11659)
OTHER INFORMATION: n is a,
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INFORMATION: n is a,
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THER INFORMATION: n is a, PEATURE:
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LOCATION: (231)..(231)
OTHER INFORMATION: n is
                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (1)..(3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
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TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)
FILE REFERENCE: 55815-0102 (319189)
FILE REFERENCE: 55815-0102 (319189)
FILE REFERENCE: 2005-11-03
FRIOR APPLICATION NUMBER: EP 04105482.6
FRIOR APPLICATION NUMBER: EP 04105483.4
FRIOR FILING DATE: 2004-11-03
FRIOR APPLICATION NUMBER: EP 04105483.4
FRIOR APPLICATION NUMBER: EP 04105485.9
FRIOR APPLICATION NUMBER: EP 04105485.9
FRIOR APPLICATION NUMBER: EP 04105485.9
FRIOR FILING DATE: 2004-11-03
FRIOR APPLICATION NUMBER: EP 04105484.2
FRIOR FILING DATE: 2004-11-03
FRIOR APPLICATION NUMBER: US 60/662,276
FRIOR APPLICATION NUMBER: US 60/662,276
FRIOR APPLICATION NUMBER: US 60/700,293
FRIOR APPLICATION NUMBER: US 60/700,293
FRIOR FILING DATE: 2005-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
13.5%; Score 94.6; DB 8; Length 20;
Best Local Similarity 82.8%; Pred. No. 5.4e-08;
Matches 120; Conservative 0; Mismatches 24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 TTTTTTTTTTGATGATTTTAATAAATATCATTTTCTT
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13.5%; Score 94.4; DB 8;
Best Local Similarity 74.4%; Pred. No. 5.7e-08;
Matches 119; Conservative 0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164203 TGTTGGTGTGCTGCACCCATTAACT 164179
      PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PATCHIN VETSION 3.3
SEQ ID NO 23277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 TGCTGGTGTGCTGCACCCATTAACT 160
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US-11-266-748A-60144
'Sequence 60144, Application US/11266748A
'Sequence 60144, Application US/11266748A
'Publication No. US20060134663A1
'GENERAL INFORMATION:
'APPLICANT: Harkin, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin version 3.3
SEQ ID NO 60144
LENGTH: 166949
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                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-23277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo Sapiens
US-11-266-748A-60144
                                                                                                                                                                                                                                                                                                                               LENGTH: 209216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   us-ii-266-748A-23277/c

Sequence 23277, Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Partick
APPLICANT: Johnston, Rarl
TILE OF INVENTION: Methods of USing the Same
TILE OF INVENTION: Methods of USing the Same
TILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulijan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT PPLLING DATE: 2005-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                531022 GTTGGTGTGCTGCATCATTAACTCA 531047
                                                                                                                                                                                                                                                                                                                  PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 0410550.0
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/602,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo Sapiens
US-11-266-748A-29045
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LENGTH: 755217
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Query Match
Best Local Similarity 87.7%;
Matches 114; Conservative
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US-11-266-748A-202832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                                                                                                           19640 İTİTİTITILÇATTİTATİTİTİTİTİTİTİTİTİTİTİTİTİTİTİTACTİTİCÜLİT 19699
                                                                                                          189 ACTITIAAGITCTAGGGTACATGTGCACAACGIGCAGGTTTGTTACATATGTATACATGT 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 ACTITITAAGITITIAGGGIACAIGIGCAAAGIGIGCAGGITAGITACAIATATATACAIGT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 IGTITCACATAAAGITITITITITITGATGATTTTAATAAAATATCATTTTCTTTTTTA
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APPLICANT: Muligan, Karl
ITILE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REPERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT APPLICATION NUMBER: EP 04105492.6
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PILING DATE: 2004-11-03
PRIOR PLLING DATE: 2004-11-03
PRIOR PLLING DATE: 2004-11-03
PRIOR PLLING DATE: 2004-11-03
PRIOR PLLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
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PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PLINGO NUMBER: ED 60/700,700
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                                                                                                                                                                                                                                                      19760 GTATACATGTGCCATGCTGCTGCTGCACCACTAACTC 19799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.4%; Score 94; DB 8; I
76.7%; Pred. No. 4.1e-08;
tive 0; Mismatches 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 50139, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 76.7
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-50139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Harkin, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 56
US-11-266-748A-202832/c
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803 TITCAACAATCACTCITITATIATIATIATIATIATIATAC-ITTAAGITITIAGGGTACA 745
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iSequence 23474, Application US/11266748A

; Sequence 23474, Application US/11266748A

; Publication No. US20660134663A1

; GENERAL INFORMATION:

; APPLICANT: Harkin, Paul

; APPLICANT: Mulligan, Karl

; TILLE OF INVENTION: Transcriptome Microarray Technology and

; TILLE OF INVENTION: Transcriptome Microarray Technology and

; TILLE OF INVENTION: Methods of Using the Same

; TILLE REFERENCE: 55815-0102 (19189)

; CURRENT FILLING DATE: 2005-11-03

; PRIOR PILLING DATE: 2004-11-03

; PRIOR FILLING DATE: 2004-11-03

; PRIOR FILLING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105507.0

; PRIOR FILLING DATE: 2004-11-03

; PRIOR FILLING DATE: 2004-11-03

; PRIOR FILLING DATE: 2004-11-03

; PRIOR FILLING DATE: 2004-11-03

; PRIOR FILLING DATE: 2004-11-03

; PRIOR FILLING DATE: 2004-11-03

; PRIOR FILLING DATE: 2004-11-03

; PRIOR FILLING DATE: 2004-11-03

; PRIOR FILLING DATE: 2004-11-03

; PRIOR FILLING DATE: 2004-11-03

; PRIOR FILLING DATE: 2004-11-03
TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: MACHINES (131948)

FILE REFERENCE: 55815-0102 (31948)

CURRENT APPLICATION NUMBER: US 04105479.2

PRIOR APPLICATION NUMBER: ED 04105482.6

PRIOR PILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

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PRIOR PELING DATE: 2004-11-03

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PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2005-03-14

PRIOR FILING DATE: 2005-03-14

PRIOR FILING DATE: 2005-07-18

PRIOR FILING DATE: 2005-07-18

PRIOR FILING DATE: 2005-07-18

PRIOR FILING DATE: 2005-07-18

PRIOR FILING DATE: 2005-07-18

PRIOR FILING DATE: 2005-07-18

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PRIOR FILING DATE: 2005-07-18

PRIOR FILING DATE: 2005-07-18
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Pred. No. 4.3e-08;
0; Mismatches 15; Indels
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misc_feature (3392) .. (3393)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334166 TITTAGGGTACACGTGCACAATGTGCAGGTTAGTTACATATGTATAATATGTGTGCCATGCTG 334225
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                                                                                                                                              Length 347503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HARTHI, Paul
APPLICANT: HARTHI, Paul
APPLICANT: HARTHI, Paul
ITLE OF INVENTION: Transcriptcome Microarray Technology and
TITLE OF INVENTION: Transcriptcome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US 0411/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-01-16
PRIOR PILING DATE: 2005-01-18
PRIOR PILING DATE: 2005-01-18
PRIOR FILING DATE: 2005-01-18
PRIOR FILING DATE: 2005-01-18
PRIOR FILING DATE: 2005-01-18
PRIOR FILING DATE: 2005-01-18
PRIOR FILING DATE: 2005-01-18
PRIOR FILING DATE: 2005-01-18
PRIOR FILING DATE: 2005-01-18
PRIOR FILING DATE: 2005-01-18
NUMBER OF SEQ ID NOS: 489996
SOFTWARE PARENTLY VERSION 3.3
                                                                                                                                                                                                                                                                                                         Query Match 13.4%; Score 93.8; DB 8; Length 3 Best Local Similarity 83.7%; Pred. No. 7.8e-08; Matches 118; Conservative 0; Mismatches 22; Indels
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-18
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
SEQ ID NO 23474
LENGTH: 347503
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US-11-266-748A-23170
Sequence 23170, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (3384)..(3384)
OTHER INFORMATION: n is a, c, g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 GTGTGCTGCACCCATTAACTC 161
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LOCATION: (3381)..(3381)
OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                  ORGANISM: Homo Sapiens US-11-266-748A-23474
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ORGANISM: Homo Sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEO ID NO 23170
LENGTH: 170452
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                                                                                                                                                                                                               TYPE: DNA
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71 TACTITITAAGITITIAGGGTACATGTGCAAAGIGTGCAGGTTAGTTACATATATATACATG 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
13.4%; Score 93.6; DB 8;
Best Local Similarity 80.3%; Pred. No. 7.9e-08;
Matches 122; Conservative 0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; LOCATION: (144156)..(144156)
; CHER INFORMATION: n is a, c, g, or t
US-11-266-748A-23170
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LOCATION: (3927)..(3927)
OTHER INFORMATION: n is a, c,
                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (3423)..(3423)
OTHER INFORMATION: n is a, c,
                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: (3406)..(3407)
CTHER INFORMATION: n is a, c
                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (3446)..(3446)
OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (3545)...(3545)
OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (3905)..(3905)
OTHER INFORMATION: n is a,
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LOCATION: (3922)..(3922)
OTHER INFORMATION: n is a,
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LOCATION: (3924)..(3924)
OTHER INFORMATION: n is a,
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LOCATION: (15605)..(15605)
OTHER INFORMATION: n is a,
LOCATION: (3392)..(3392)
OTHER INFORMATION: n is a,
                                             NAME/KEY: misc feature
LOCATION: (3400)..(3400)
OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (3909)..(3909)
OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (3907)..(3907)
OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (3907)..(390
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
SEQ ID NO 200176
LENGTH: 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 GGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             871 GGTGTGCTGCACCCATTAACTC 850
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SOFTWARE: Patentin version 3.3
SEQ ID NO 60803
LENGTH: 176928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 83.1
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
i LOCATION: (24476);
CTHER INFORMATION: n is a,
US-11-266-788A-60803
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CORGANISM: Homo Sapiens
US-11-266-748A-200176
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ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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                                                                                  JULIATOR 148A-1901/C
Sequence 29041/C
Sequence 20041/C
Sequence 20041/C
Sequence 20041/C
Sequence 20041/C
Sequence 20041/C
Sequence 20041/C
Separation No. US2006013466341
Sebalication No. US2006013466341
Separation No. US2006013466341
Separation Sequence 200411001
Separation Sequence 300411001
Separation Sequence 3005-11-03
Separation Separation NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
SPRIOR FILING DATE: 2004-11-03
SPRIOR FILING DATE: 2004-11-03
SPRIOR SPELICATION NUMBER: EP 04105482.6
SPRIOR FILING DATE: 2004-11-03
SPRIOR FILING DATE: 2004-11-03
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Sequence 200176, Application US/11266748A

PUDLIcation No. US20060134663A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Mulligan, Karl

TITLE OF INVENTION: Transcriptome Microarray Techr

TITLE OF INVENTION: Methods of Using the Same

FILE REPRENCE: SSB15-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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Best Local Similarity 86.6%;
Matches 103; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo Sapiens
US-11-266-748A-29041
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LENGTH: 1237661
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80 GITTIAGGGIACATGTGCAAAGTGTGCAGGTTAGTTACATATATATACATGTGCCATGCT 139
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                                                                                                                                                                                                                                                                                                                                                                                                              931 GTTTTAGGGTACATGTGCACAACATGCAGGTTAGCTACATATGTATACATGTGCCCATGTT
                                                                                                                                                                                ۲;
13.3%; Score 93.2; DB 8; Length 1000; 83.1%; Pred. No. 5.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JULIATOR Y848-0803
Sequence 60803, Application US/11266748A
Publication No. US20060134663A
FEBRERGE INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
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TITLE OF INVENTION: WUMBER: BP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: BP 04105482.6
PRIOR APPLICATION NUMBER: BP 04105483.4
PRIOR PELING DATE: 2004-11-03
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PRIOR PELING DATE: 2005-03-14
                                                                                        23; Indels
                                                                                            0; Mismatches
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Score 93.2; DB 8; Length 176928; Pred. No. 9.3e-08; 0; Mismatches 33; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 909203;
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US-11-266/148A-29039
Sequence 29039
Sequence 29039
Sequence 29039
Sublication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
CURRENT APPLICATION NUMBER: EP 0410549.2
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PELING DATE: 2004-11-03
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                                                                                                                                                                                                                                                                                                                                                                                                           102604 AAACATGTGCCATGCTGGTGTGCACCACTAACAC 102641
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                                                                                                                                                                                                                                                                                                                                                                              124 ATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
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Pred. No. 1.1e-07;
0; Mismatches 33;
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78.1%;
Query Match
13.3%;
Best Local Similarity 78.5%;
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.3
Best Local Similarity 78.1
Matches 125; Conservative
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US-11-266-748A-29039
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RESULT 63 US-11-266-748A-211402

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APPLICANT: CAVALEC, MALLE.
APPLICANT: CALMAROV, IIya
APPLICANT: Chumakov, IIya
APPLICANT: Chumakov, IIya
APPLICANT: Chumakov, IIya
APPLICANT: Gestenaves, Benoit
APPLICANT: Gordriner, Cacherine
APPLICANT: Blas, Isabelle
TITLE OF INVENTION: TREATMENT OF MENTAL DISORDERS
FITLE OF INVENTION: TREATMENT OF MENTAL DISORDERS
FILE REFERENCE: G-1940S03PCT
CURRENT APPLICATION NUMBER: US 10/519,335
FILE REFERENCE: G-1940S03PCT
CURRENT APPLICATION NUMBER: US 60/391,359
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-25
SOFTWARE: Patentin version 3.1
SEQ ID NO 37
LENGTH: 151830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 TITITITITITITITITITITITITATITATIATAC-TITIAAGTITITIAGGGTACATGTGCACAATGTGCAG
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                                                                                                       APPLICANT: HARKIN, Paul
APPLICANT: HARKIN, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Uniligan, Karl
ITLE OF INVENTION: Transcriptome Microarray Technology and
ITLE OF INVENTION: Methods of Using the Same
ITLE OF INVENTION: Methods of Using the Same
FILE REPERENCE: 58815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
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PRIOR PILING DATE: 2005-01-18
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
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Pred. No. 6.1e-08;
0; Mismatches 5; Indels
Sequence 211402, Application US/11266748A bublication No. US20060134663A1 GENERAL INFORMATION:
APPLICANT: Harkin, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-519-335-37
; Sequence 37, Application US/10519335
; Publication No. US20060099210A1
; GENERAL INFORMATION:
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Best Local Similarity 94.7%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo Sapiens
US-11-266-748A-211402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 211402
LENGTH: 607
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                                           NAME/KEY: misc feature
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FEATURE:
NAME/KEY: misc_feature
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...TON: (5363) .. (536
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NAME/KEY: misc_feature
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LOCATION: (141674)..(141674)
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LOCATION: (118900)..(118900)
OTHER INFORMATION: n = a or c or g
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LOCATION: (119123)..(119123)
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LOCATION: (98209)..(98209)
OTHER INFORMATION: n = a or c or
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LOCATION: (109094)..(109094)
THER INFORMATION: n = a or c or
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LOCATION: (119024)..(119052)
OTHER INFORMATION: n = a or c or
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LOCATION: (119053)..(119112)
VTHER INFORMATION: n = a or c or
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LOCATION: (142063)..(142063)
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143163 AGGGTACATGTGCATAATGTGCAGGTTTGTTACATATGTATACATGTGTGTCATGTTGGTGT 143104
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APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
ITILE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 5815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFFWARE: PATENTIN VERSION 3.3
SEQ ID NO 22833
LENGTH: 319486
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.3%; Score 93; DB 8; Length 168545; Best Local Similarity 84.7%; Pred. No. 1e-07; Matches 116; Conservative 0; Mismatches 20; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 13.3%; Score 93; DB 8; Length 319486; Best Local Similarity 77.6%; Pred. No. 1.1e-07; Matches 125; Conservative 0; Mismatches 35; Indels 1
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR PILING DATE: 2005-03-14
PRIOR PELING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SEQ ID NO 59086
LENGTH: 168545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22833, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
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US-11-266-748A-22833
                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-59086
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US-11-266-7484-59086/C

j Sequence 59086, Application US/11266748A

j Publication No. US20060134663A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Muligan, Rarl

TITLE OF INVENTION: Transcriptome Microarray Technology and

TITLE OF INVENTION: Transcriptome Microarray Technology and

TITLE OF INVENTION: Transcriptome Microarray Technology and

TITLE OF INVENTION: Transcriptome Microarray Technology and

TITLE OF INVENTION: 2019199)

FILE REFERENCE: 55815-0102 (319189)

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105492.6

PRIOR PILING DATE: 2004-11-03

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13.3%; Score 93; DB 6; Length 151830;
Best Local Similarity 77.6%; Pred. No. 1e-07;
Matches 125; Conservative 0; Mismatches 35; Indels 1
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SOFTWARE: Patentin version 3.3
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ORGANISM: Homo Sapiens
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                                                         61651 CTGTCCGCAAAACATTCTTTTTTTTTTTTGGTCTTTATTATTATTATTATTATTATTATT
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APPLICANT: Activation, Partick
APPLICANT: Mulligan, Karl
ITILE OF INVENTION: Transcriptome Microarray Technology and
TTILE OF INVENTION: Methods of Using the Same
TTILE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105402.6
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105405.9
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-01-18
PRIOR FILING DATE: 2005-01-18
PRIOR FILING DATE: 2005-01-18
PRIOR FILING DATE: 2005-01-18
PRIOR FILING DATE: 2005-01-18
PRIOR APPLICATION NUMBER: US 60/700,293
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                                                                                                                                                                                                                               61770 TGTATACAGGTGCCATGATGGTGTGCTGCATCCATTAACTC 61810
                                                                                                                                                                                          TATATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
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Pred. No. 6.9e-08;
0; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                                              US-11-266-748A-200842/c
Sequence 200842, Application US/11266748A
PUBlication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
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APPLICANT: Harkin, Paul APPLICANT: Johnston, Patrick APPLICANT: Mulligan, Karl
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Best Local Similarity 78.8°
Matches 123; Conservative
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US-11-266-748A-200842
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US-11-266-748A-25022
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TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR PELING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR PILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

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PRIOR PELING DATE: 2005-01-14

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APPLICANT: Holigan, Karl
TITLE OF INVENTION: Transcriptcome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Wethods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: US 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
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PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
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Pred. No. 9.6e-08;
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APPLICANT: Harkin, Paul
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89.3%;
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Matches 100; Conservative
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20085 TITTITITITIATIALC-TCTAAGITTITAGGGTACATGTGCACATTGTGCAGGTTAGTTACATA 20143
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                                                                                                                                                                                                                                                                                                                                1;
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13.2%; Score 92.6; DB 8; Length 39638;
Best Local Similarity 72.7%; Pred. No. 1e-07;
Matches 133; Conservative 0; Mismatches 49; Indels 1;
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APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
FIGUREANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 5815-0102 (319189)
CURRENT FILING DATE: 2005-11-03
FRIOR APPLICATION NUMBER: EP 04105482.6
FRIOR FILING DATE: 2004-11-03
FRIOR PAPLICATION NUMBER: EP 04105482.6
FRIOR PELLING DATE: 2004-11-03
FRIOR APPLICATION NUMBER: EP 04105483.4
FRIOR PELLING DATE: 2004-11-03
FRIOR PELLING DATE: 2004-11-03
FRIOR APPLICATION NUMBER: EP 04105485.9
FRIOR PELLING DATE: 2004-11-03
FRIOR PELLING DATE: 2004-11-03
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FRIOR FILING DATE: 2004-11-03
FRIOR PELLING DATE: 2004-11-03
FRIOR FILING DATE: 2004-11-03
FRIOR FILING DATE: 2004-11-03
FRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
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US-11-266-748A-60803
; SEQ ID NO 23809
; LENGTH: 39638
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-23809
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ORGANISM: Homo Sapiens
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AQ229797 HS 2033\_A AQ109589 CIT-HSP-2 AI310239 GO75h12.x BC010517 HOMO SADI B72257 RPCII1-7016

Searched:

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Result õ

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BX415806 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP008YE09 3-PRIME, mRNA sequence.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases I to 961)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
Unpublished (2001)
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                                              AA344409
CA947015
AQ052012
AL601657
AQ266524
AG189910
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AA446110
AQ029723
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
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BS2311 CIT-HSP-388
AQ356702 CITBI-E1-
AQ195233 RPCI11-48
BB349127 BB349127
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DA104597 DA104597
AQ102621 PRI LYOGI
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AQ756779 HS_5407 A
CZ457195 MCF-40G11
CR373797 CR737970
AQ021610 CIT-HSP-2
CB048927 NISC_ICI
                                            July 19, 2006, 06:54:08; Search time 4403 Seconds (without alignments) 8890.196 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                       96473596
     GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                         US-10-661-966-1_146001-146700_A146311
                                                                                                                        48236798 segs, 27959665780 residues
                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                              Maximum Match 100%
Listing first 70 summaries
                                - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                             B52311
A0356702
A019523
DB349127
A011354
CX869873
DA104597
AQ84211
AQ84211
AQ27159
W44804
AQ756779
CZ457195
CR737970
CB410332
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                                                                                                   IDENTITY NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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90 est3...

90 est6...

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90 htc...

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90 est8...
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Perfect score:
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                                OM nucleic
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CR959536 HOMO SADIO CR450878 MCP731M05 AA344405 SET5031 AA344405 SET5031 AA266524 RPC7111-53 AA169910 Pan trog1 B92240 RPC711-20K1 B92240 RPC711-20K1 B92240 RPC711-12 AQ07657 UI-H-EIO-B92249 AGECOURT-AQ0319769 RPC711-11 AQ079743 HS SF71 AQ02973 RPC711-14 DB302517 DB302517 AQ02973 RPC711-11 AQ02973 RPC711-11 AQ02973 RPC711-11 AQ02973 RPC711-11 AQ02973 RPC711-11 AQ02973 RPC711-11 AQ02973 RPC711-11 AQ02973 RPC711-11 AQ02973 RPC711-11 AQ02973 RPC711-11 AQ028464 HOMO SADI AQ07761 RF-FNO AZ519511 RPC7-11-3 BX115372 AQ65813 RPC711-1211 CR558489 HOMO SADI AQ628311 CTPRI-EI-CR558489 HOMO SADI AQ628311 CTPRI-EI-CR558489 HOMO SADI AQ13171 RPC711-1211 CR750736 BXF70470 AF118407 AF118407 AF118407 AF118407 AF118417 AF118407 AF118407 AF118407 AF118407 AF118407 AF118407 AF118407 AF118407 AF118407 AF118407 AF118407 AF118407 AF118407 AF118407 AF118407

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B52311 522 bp DNA linear GSS 20-JUN-1998 CIT-HSP-388D1.TR CIT-HSP Homo sapiens genomic clone 388D1, genomic
                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pECBAC1; Site_1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                455 TGCTGGTGTGCTGCACCCATTAACTGTCATTTAGCATTACAAAATTTCTTAACCTTT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 TGCTGGTGTGCTGCACCCATTAACTCACATGAAGTTTTTTTAAATTTTAGTGACAGTTT 195
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Seg primer: M13 Reverse
Class: BAC ends.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Adams, M.D., Rounaley, S.D., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building
Unpublished (1997)
                                                                                                                                                                                                                                                                                       /clone_lib="Human MCF7 breast cancer cell line library
(MCF7 ])"
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Contect: Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdddams@tigr.org
                                                                                                                             /organism="Homo sapiens"
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                                                                                                                                                                                                                          /sex="female"
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http://www.genomex.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     procedure.
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Matches 138; Conservative
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                     Contract: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime
end enriched, double-serrand cDNA was digested with Not I and Cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1683.f
For more information about this cluster; see
http://www.genoscope.cns.fr/cdna?e=CSOCAPDO8ACOSNP1&c=1683.f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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May 15, 2003 this sequence version replaced gi:30765544.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 TGCTGGTGCTGCACCCATTAACTC 820
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AQ195233 632 bp DNA linear GSS 20-APR-1999
RPCIll-48C19.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-48C19,
                                                                                                                                                                                                121 TTAAGTTTTTAGGGTACATGTGCACAACGTGCAGGTTTGTTACATATGTATACATGTGCCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae, Homo.

1 (bases I to 632)
Adams, M.D., Rounaley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, B., Wible, C., de Jong, P. and Venter, J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
Other GSSs: RPCIII 48C19.TK
Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: or dealy solutions are derived from the human BAC library RPCI-11. For BAC Clones are derived from the human BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html class: BAC ends.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell type="Lymphocytes"
/clone lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
                                                                                                           8 ACAIAAAGITTTTTTTTTTTGATGATTTTTAAIAAAAIATCATTTTCTTTTTTTTTATTA
                      Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 14.7%; Score 102.8; DB 11; Length 632; Best Local Similarity 82.3%; Pred. No. 2.9e-08; Matches 130; Conservative 0; Mismatches 27; Indels 1;
                                                                  27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                      Score 102.8; DB 11;
Pred. No. 3e-08;
                                                                  0; Mismatches
                         Score 102.8;
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mol_type="genomic DNA"
/mb_xref="GDB:7518114"
/db_xref="taxon:9606"
/clone="RPCI-11-48C19"
                                                                                                                                                                                                                                                                                        136 TGCTGGTGTGCTGCACCCATTAACTC 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genomic survey sequence.
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AQ195233.1 GI:3606845
                         14.7%;
81.5%;
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                                                                Matches 119; Conservative
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                                             Similarity
                      Query Match
                                                Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 bp DNA linear GSS 24-JAN-1999 CITBL-E1-2531H1.TR CITBL-E1 Homo sapiens genomic clone 2531H1, genomic survey sequence.
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1 (bases 1 to 375)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
Map Building
                                                                                                                                                                                                                                                                                                          Ή.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
Other GSSs: CITBI-E1-2531H1.TF
Contact: Shaying Jaho, William Nierman, Mark Adams
Contact: Shaying Jaho, William Nierman, Mark Adams
Contact: Shaying Jaho, William Nierman, Mark Adams
Department of Eukaryotic Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0208
Fax: 301 838 0208
Email: hbeepigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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/clone_lib="CITBI-B1"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
                                                                                                                                                                                                                                                                                                                                                   16 TITITITITITIGATGATTITAATAAAATATCATTITCTTTTTTTTATTATAATACTT
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                              /cell type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
                                                                                                                                                                                                                                                                                                          1,
                                                                                                                                                                                                                                                                 DB 11; Length 522;
                                                                                                                                                                                                                                                              Score 106.8; DB 11; Length
Pred. No. 5.8e-09;
0; Mismatches 17; Indels
'organism="Homo sapiens"
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/organism="Homo sapiens"
                    /mol_type="genomic_DNA"
/db_xref="GDB:5379775"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 TGCTGGTGTGCTGCACCCATTAACTC 395
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/db_xref="taxon:9606"
/clone="2531H1"
                                                           /db_xref="taxon:9606"
/clone="388D1"
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                                                                                                                                                                                                                                                            15.3%;
87.7%;
                                                                                                           sex="Male"
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                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 87.7'
Matches 128; Conservative
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tch 14.6%; al Similarity 77.8%; 123; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .397
                                                                                                                                                                                               Hominidae; Homo.
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FLJ Project (HRI Team)

Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-ddha@hifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, K., Wakamatsu, A., Sekine, M., Tsuritani, K., Wakaguri, H., Sekine, M., Tsuritani, K., Wakaguri, H., Yoneyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishidashi, T., Takahashi-Fulii, A., Tanasse, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative
                                                                                                                                                                                                                   EST 04-DEC-2005
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                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                    421 ATGTGCCATGCTGGTGCACTGCACCATCTATTCCCCT 458
                                                                              128 ATGTGCCATGCTGGTGTGCTGCACCCATTAACTCACAT 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="trachea"
/clone lib="TRACH3"
/note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Matches 108; Conserv
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DB349127
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RESULT 7 AQ111354

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CX869873 506 bp mRNA linear EST 03-FEB-2005 HESC4 38 E04.gl A037 NIH MGC 262 Homo sapiens cDNA clone IMAGE:7474642 57, mRNA sequence.
AQ111354 190-2382A15.TR CIT-HSP Homo sapiens genomic clone 2382A15,
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                                                                                                                                                                                                                                                                                                                                        Venter, J.C.

Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
Unpublished (1998)
Other GSSs: CIT-HSP-2382A15.TF
Contact: Mark Adams
Contact: Mark Adams
The Institute for Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fex: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 ificrrrrrrrrrcrifititititititicreditialiritaliritalirialirialirali 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                      1 (bases 1 to 397)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.
Berry, K., Granger, D., Suh, B., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 ATACATGCCATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 102; DB 11;
Pred. No. 4.1e-08;
0; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="2382A15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                  genomic survey sequence.
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CX869873.1 GI:58553047
                                                                                                AQ111354.1 GI:3488011
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KEYWORDS
SOURCE
ORGANISM
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Hominidae, Homo.

I (bases 1 to 552)

Kiuura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,

Kiuura, K., Wakamatsu, A., Sekine, M., Tsuritani, K., Wakaguri, H.,

Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,

Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,

Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,

Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.

Diversification of Transcriptional Modulation: Large-scale

Identification and Characterization of Putative Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS 09-NOV-1999
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 421)
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HS_5499_B1_G04_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=9267 Col=7 Row=N, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
14.6%; Score 102; DB 9; Length 552;
Best Local Similarity 85.6%; Pred. No. 4e-08;
Matches 125; Conservative 0; Mismatches 20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="cerebellum"
/clone Tib="BRACE3"
/note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                 Genome Res. 16 (1), 55-65 (2006)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="BRACE3018053"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLJ Project (HRI Team)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
                       sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .552
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                                                                                                                                                     REFERENCE
                                                                                                                                                                             AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue type="embryonic stem"
/cell type="human embryonic stem cells"
/cell type="human embryonic stem cells"
/cell type="human embryonic stem cells"
/clone lib="NIH MGC 262"
/note="Vector: pExpress-1; Site_1: Not1; Site_2: EcoRV;
RNA obtained from human embryonic stem cells isolated from the inner cell mass of blastocyst stage embryos and differentiated to an early neural progenitor cell type.
Cell line id and NIH Registry designation is BGO1.
Positive for Nestin and Musashi expression. Passage number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DA104597 EST 02-NOV-2005
DA104597 BRACE3 Homo sapiens cDNA clone BRACE3018053 5', mRNA
                                                                                                           Contact: Daniels S. Gerhard, Ph.D.

Contact: Daniels S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 RmL0A07 Bethead, MD 20892

Email: cgapbs-romail.nih.gov

Tissue Procurement: Bresagen, Inc.

CDNA Library Preparation: Express Genomics, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Laboratory for Genomics and Bioinformatics,

University of Georgia

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.lnl.gov

Plate: LLAM15783 row: i column: 08

Seq primer: JENREV (CAGGAAACAGCTATGACC)

High quality sequence stop: 506.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18. cDNA primed using oligo-dT primer:
5'-pGACTAGTTCTAGATCGCGAGCGCCCCCT(7)25-3' and cloned into
the ECORV/NotI sites of pExpress-1. This primary library
is non-normalized (normalized primary library is
NIH MGC 259). It was constructed by Express Genomics
(Frederick, MD). Sequence ends have been trimmed to
exclude vector and regions below Phred quality 16. Note:
this is a Mammalian Gene Collection library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 506)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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0; Mismatches 20
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="IMAGE:7474642"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
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DA104597.1 GI:78759434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex="male"
                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 125; Conservative
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Homo sapiens
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KEYWORDS
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AQ527159
  JOURNAL
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                                                                                                                                Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-38618
Fax: (206) 616-38618
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Seq primer: 9267 row: N column: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site 1: EcoR1; Site 2: EcoR1;
Male blood DNA was isolated from one randomly chosen donor and partially disested with a combination of EcoR1 and EcoR1 Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoR1 sites"
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AG102621 681 bp DNA linear GSS 03-NOV-200:
Pan troglodytes DNA, clone: PTB-105P19.F, genomic survey sequence.
AG102621
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 ITTICITITITIATTATTATTATACTTTTAAGTTTTAGGGTACATGTGCAAAGTGTGCAG
                                                           Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Taylor, T.D., Yada, T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.5%; Score 101.8; DB 11; Length 421;
llarity 93.8%; Pred. No. 4.5e-08;
Conservative 0; Mismatches 7; Indels 0;
                                                                                 scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
|mol_type="genomic DNA"
|db_xref="taxon:9606"
|clone="plate=9267 Col=7 Row=N"
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class: BAC ends
High quality sequence stop: 421.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 681)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .421
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es 106; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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AG102621
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AQ527159 591 bp DNA linear GSS 18-MAY-1999 CITBI-E1-260411.TF CITBI-E1 Homo sapiens genomic clone 260411, genomic survey sequence.
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Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the RkD process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239
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Seg primer: M13-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
|cell_type="lymphoblast"
|clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 101.8; DB 14; Length
Pred. No. 4.3e-08;
0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 TTTTTTTTTGATGATTTTAATAAATATCATTTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | . .681
| /organism="Pan troglodytes"
| mol_type="genomic_DNA"
| /db_xref="taxon:9598"
| /clone="PTB-105P19.F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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AQ527159.1 GI:4838919
                                                                                                                                                                                                                                                                                                                                                    clone tracking errors.
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Best Local Similarity 81.4%;
Matches 118; Conservative
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Class: BAC ends
High quality sequence stop: 527.
Location/Qualifiers
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GSS.
                                                                                                                                                                                                                                                                                                   14.5%;
78.1%;
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Homo sapiens
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Best Local S
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AQ756779
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W44804 11 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone IMAGE:320896 3' similar to contains L1.t3 L1 repetitive element;
                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="sperm"
/clone_lib="CITBI-E1"
/note="Wector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
                                                                                                                                                                                                                                                                                                                    75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae, Homo.

1 (bases 1 to 242)

1 (bases 1 to 242)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hutan, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                             14.5%; Score 101.4; DB 11; Length 591; 81.8%; Pred. No. 5.1e-08;
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:320896"

Lissue type="parathyroid tumor"

Adev stage="adult"

/lab_host="DHIOB (ampicillin resistant)"
                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                               Pred. No. 5.1e-08;
0; Mismatches 26
              Location/Qualifiers
1. 591
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1258554"
/db_xref="taxon:9606"
                                                                   /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="260411"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: mob.REGA+ET
High quality sequence stop: 233.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 TGCTGGTGCTGCACCCATTAA 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W44804.1 GI:1328887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                       /sex="male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                               Conservative
BAC ends
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Class:
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3868
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieteracedejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                          TTTTT3'], doubte-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTTT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Farima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."
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1 (bases 1 to 527)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 ATTATACTTTTAAGTTTTAGGGTACATGTGCACAATGTNAGCGTTAGTTACATATGTATA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQ756779 1inear GSS 27-JUL-HS 527 bp DNA linear GSS 27-JUL-HS_5407_A2_G12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=983 Col=24 Row=M, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence-tagged connectors: A sequence approach to mapping and
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 242;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 101.2; DB 10
Pred. No. 5.9e-08;
0; Mismatches 34,
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Seg primer: T7
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CR737970 CR737970 Homo sapiens library (Ebert L) Homo sapiens cDNA clone IMAGE9998C11359; IMAGE:190402 5', mRNA sequence.
constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 ratitacaaaatagiriririringactrigtarcirtartratriarrirariraatia 311
                                                                                                                                                                                                                                                                                            This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
121: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
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/db_xref="taxon:9606"
/clone="IMAGp998C11359 ; IMAGE:190402"
/clone_lib="Homo saplens library (Ebert L)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neubert, P.,
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                                                                                                                                                                  37; Indels
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KZZPD; INAGD999EC11359.
RZPDLIB; IN.A.G.E. cDNA Clone Collection;
Concact: Inge Arlart
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                                                                                                                     Score 100.8; DB 1
Pred. No. 6.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 746)
Ebert, L., Heil, O., Hennig, S., Korn, B.,
Peters, M., Radelof, U. and Schneider, D.
I.M.A.G.E. CDNA (lone Collection
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heubnerweg 6, D-14059 Berlin, Germany
                                                                                                                                                               0; Mismatches
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    746
    organism="Homo sapiens"

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                                                                                                                       14.4%;
76.9%;
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                                                                                                                                              Best Local Similarity 76.9
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 83.8
Matches 114; Conservative
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                                                                                                                       Query Match
Best Local Similarity
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CR737970
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                                                                                                                     /sex="male"
/clone lib="RPCI-11 Human Male BAC Library"
/clone lib="RPCI-11 Human Male BCORI; Site 2: ECORI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of ECORI and
ECORI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at ECORI sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae, Homo.

1 (bases 1 to 445)
Voliks.V., Raphael, B.J., Huang, G.-O., Murnane, J., Brebner, J.H.,
Bajaarowicz, K., Paris, P., Tao, Q., Kowbel, D., Lapuk, A.V., Kuo, W.-L.,
Shagin, D.A., Shagina, I.A., Magrane, G., Gray, J.W., Jan, F.-C., de
Jong, P., Pevraer, P. and Collins, C.

Becoding the genomic architecture and high throughput detection of
Fusion transcripts in breast cancer cell lines: implications for a
tumor genome project
Unpublished (2005)
Contact: Volik SV
                                                                                                                                                                                                                                                                                                                                                            ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CZ457195 445 bp DNA linear GSS 20-OCT-2 MCF740G11TR Human MCF7 breast cancer cell line library (MCF7_1) Homo sapiens genomic clone MCF7_40_G11, genomic survey sequence. CZ457195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="Human MCF7 breast cancer cell line library (MCF7_1)"
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                              Score 101.2; DB 11; Length 527; Pred. No. 5.6e-08; 0; Mismatches 30; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 GTATACATGTGCCATGCTGTGTGCTGTACCCATTAACTC 231
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This clone is available from Amplicon Express http://www.genomex.com
Class: BAC ends.
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UCSF Box 0808, San Francisco, CA 94143-0808,
Tel: 415 502 7066
Fax: 415 502 5665
                                   /organism="Homo sapiens"
|mol_type="genomic DNA"
|db_xref="taxon:9606"
|clone="Plate=983 Col=24 Row=M"
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/db_xref="taxon:9606"
/clone="MCF7_40_G11"
/sex="female"
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Best Local Similarity 80.6%;
Matches 129; Conservative (
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CZ457195
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CB048927.1 GI:27787214
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                                                                                                 Homo sapiens (human)
                                                                                                                  Homo sapiens
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                                                                                                                                                           AQ021610 417 bp DNA linear GSS 09-JUN-1998 CIT-HSP-2311P19.TR CIT-HSP Homo sapiens genomic clone 2311P19,
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                                                                                                                                                                                                                                                                                                                                Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Mark Adams
Department of Eukaryotic Genomics
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
318 AGGTTACATGCGCACAATGTGCAGGTTTGTTACATATGTATACATGTGCGTGTTGGTGT 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: Ml3 Reverse
Class: BAC ends.
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                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="Sperm"
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 100.6; DB 11; Length 417;
Pred. No. 7.3e-08;
0; Mismatches 29; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 ATATACATGTGCCATGCTGGTGTGCTGCACCCATTAACT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 GTATACATGTGCCATGCTGGTGCGCTGCACCCACTAACT 260
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Unpublished (1998)
Other GSSs: CIT-HSP-2311P19.TF
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/db_xref="taxon:9606"
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GSS.
                                                 145 GCTGCACCCATTAACT 160
                                                                378 GCTGCACCCATTAACT 393
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Best Local Similarity 81.1%;
Matches 129; Conservative 0
                                                                                                                                                                                                                                                         Homo sapiens (human)
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KEYWORDS
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ORGANISM
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AQ021610
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RESULT 18 CB048927/c

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC) Clone distribution: NCI-CGAP clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@lingge.lln.gov Plate: LLAM8007 row: L column: 19
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CB410332
CB410332.1 GI:29167072
EST.
CB048927 225 bp mRNA linear EST 17-JAN-2003
NISC gj07f10.y1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3271074
5', mRNA sequence.
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                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: LLAM8007 row: L column: 19
Seq primer: M13RP1 reverse primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3271074"
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VERSION
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1. .285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 TGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 285.
Location/Qualifiers
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AQ109589.1 GI:3486279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="male"
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AQ109589
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AUTHORS
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/mol_type="mRNA"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="twAGE:576426"

/ds tage="6 weeks postconception"

/dab_host="DH108"

/clone lib="CocGENE & MAX"

/note="Vector: pAMP1; cDNA primed using oligo-dT primer,

directionally cloned into UDG sites of pAMP1. Size

selected for insert sizes ranging from 0.2-1.8 kb.

Normalized to CocE. Primary library, non-amplified.

Library constructed by M. Lovett. For more information on

this library, please contact R. Tidwell (Washington

University) or visit the COGENE website at

http://hg.wustl.edu/COGENE/."
                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation:
CDNA Library Preparation:
CDNA Library Arrayed by: The I.M.A.G.B. Consortium/LLNL
DNA Sequencing Center (NISC)
Sequencing Center (NISC)
Clone distribution: NISC)
Clone distribution: NG-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
Info@image.llnl.gov
Plate: LLAM12849 row: B column: 11
Seq primer: M13RP1 reverse primer (ABI).
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 285)
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HS_2033_A2_F09_T7_CIT_Approved Human Genomic Sperm Library D Homo
Rapiens genomic clone Plate=2033 Col=18 Row=K, genomic survey
                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                             Hominidae; Homo.
1 (bases 1 to 23)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 TIAAGITITIAGGGIACATGTGCACGATGTGCAGGTTAGTTACATACGTATACATGTGCCA
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AQ229797.1 GI:3655026
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Homo sapiens
                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
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Matches 124; Conserv
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AQ229797
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ109589 451 bp DNA linear GSS 29-AUG-1998 CIT-HSP-2373020.TR CIT-HSP Homo sapiens genomic clone 2373020, genomic survey sequence.
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Outles Of a random human BAC End Sequence Database for Sequence-Ready
Unpublished (1998)
Outles GSSS: CIT-HSP-2373020.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
Tel: 301 838 0200
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Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                    Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 10449764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 TITITITITITIGATGATITITAATAAAATATCATTITCTTTTTTTTTATTATTATAATACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="CIT Approved Human Genomic Sperm Library /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones i E-Coli DH10B"
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                                                                                                                                                                                                               Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2031 row: K column: 18
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol type="genomic DNA"
/db xref="taxon:9606"
/clone="Plate=2033 Col=18 Row=K"
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/tissue type="2 pooled tumors (clear cell type)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 TGCTGGTGTGCTGCACCACTAACTC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 TGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BC010517.1 GI:14714746
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1 (bases 1 to 1577)
Strausberg, R.
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JOURNAL
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SOURCE
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIANL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 614 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 10cation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                          ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 01-FEB-1999
               Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 İCİTİTİTIRITİRITİRİTİTATITATITATİTİRİTİRATİTİRİTİRİTATIATAC-İ 180
                                                                   http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A1310239 541 bp mRNA linear EST 01-FEB-19: qo75h12.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1914407 3'.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 541)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                           /cell type="Sperm"
/cell type="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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Pred. No. 7.8e-08;
0; Mismatches 21; Indels 1;
                                                                                                                                                  1. .451
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db xref="taxon:9606"
/clone="2373020"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 TGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI310239.1 GI:4005110
                                                                                                                                                                                                                                                                                                                                                                                14.3%;
84.9%;
                                                                                                                                                                                                                                                   /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
Fax: 301 838 0208
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. Library
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HTC 04-MAR-2003
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Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (10-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 19 Row: a Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein
This clone has the following problem: retained intron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                           constructed by Bento Soares and M. Fatima Bonaldo.
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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                            21; Indels
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                                                                                                                                                                                                                                                                                                                                                               14.3%; Score 100.4; DB 1, 84.9%; Pred. No. 7.8e-08; iive 0; Mismatches 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1577 bp mRNA
Homo sapiens, clone IMACE:4150580, mRNA.
BC010517
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derived from Pieter J. de Jong library RPCI-11;
derived from Pieter J. de Jong library RPCI-11;
http://www.rzpd.de/cgi-bin/products/Cdl.cgi/Clone1D=RZPDB737B122008D
http://www.rzpd.de/cgi-bin/products/Cdl.cgi/Clone1D=RZPDB737B122008D
http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=737
http://www.rzpd.de/products/genomicset/
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: 449 30 32639 111
www.rzpd.de
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                                                                                                                                                                                                                                                                  94 GTGCAAAGTGTGCAGGTTAGTTACATATACATGTGCCATGCTGGTGTGCTGCACCC 153
                                                                                                                                                                                                                                                                                                                                                                                     468 GTGCACAATGTGCCTGCATGTTACATATGTATACATGTGCAAAGTTGGTGCTGCTGCACCC 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CR959536 10-JUN-200 Homo sapiens BAC end sequence of RZPDB737B122008D from genomic library (orig. Pieter J. de Jong library RPCI-11), genomic survey
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (07-JUN-2005) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 515, D-69120 Heidelberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available from RZPD;
Contact RZPD (customer.service@rzpd.de) for further information.
Clone distribution: http://www.rzpd.de/products/genomicset/
Seg-primer: T7 (TAA-TAC-GAC-TCA-CTA-TAG-GG)
Class: BAC ends.
/note="Vector: pBACe3.6; Site 1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                   34 TITAATAAAAIAICAITITCITITITIAITAATAATAATATTAAGTITITAGGGTACAI
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Schwarz,F., Neubert,P., Schneider,D., Peters,M. and Korn,B.
Direct Submission
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/note="Vector: pBACe3.6; RPCI-11 Human Male BAC
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                                                                                                                   Score 100.2; DB 11; Length 572; Pred. No. 8.4e-08;
                                                                                                                                                                             18; Indels
                                                                                                                                                                             0; Mismatches
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/db_xref="taxon:9606"
/clone="RZPDB737B122008D"
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CR959536.1 GI:66957023
                                                                                                                      14.3%;
86.0%;
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                                                                                                                                                                                Matches 111; Conservative
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1 (bases 1 to 572)

8 Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Use of BAC End Sequences for Sequence-Ready Map Building
Use of BAC End Sequences for Sequence-Ready Map Building
Use of BAC End Sequences for Sequence-Ready Map Building
Use of BAC End Sequences for Sequence-Ready Map Building
Use of BAC End Sequences for Sequence-Ready Map Building
Use of BAC End Sequences for Sequences
The Institute for Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Fax: 301 838 0208
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RPCIII-7016.TV RPCI-11 Homo sapiens genomic clone RPCI-11-7016,
B72257
                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:4150580"
/tissue_type="Brain, glioblastoma with EGFR amplification"
/clone_lib="NCI CAP—Brn64"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 ITAAGITITIAGGGTACATGTGCAAAGTGTGCAGGTTAGTTACATATATACATGTGCCA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                   21; Indels
                                                                                                                                                                                                                                                                                                                                                          DB 6;
                                                                                                                                                                                                                                                                                                                                                          Score 100.4; DB 6
Pred. No. 7.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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clone_lib="RPCI-11"
                                                               /organism="Homo sapiens"
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/db_xref="GDB:7502655"
/db_xref="taxon:9606"
/clone="RPCI-11-7016"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 TGCTGGTGTGCTGCACCCATTAACTC 161
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      Location/Qualifiers
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Best Local Similarity 84.9%;
Matches 124; Conservative
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Homo sapiens
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B72257
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Bult, C.J., Lee, N. H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Cliar, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzlugh, W.M., Fitzchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-T., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shriep, R., Bednarik, D.P., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Frenzie, A., Fischer, C., Hastings, G.A., Kozak, D.-E., Keng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Maissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Li, H., Maissner, P.S., Olsen, H., Fraser, C.M., and Venter, J.C., Intial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence
                                                                                                                                                         AA344409 307 bp mRNA linear EST 21-APR-1997
EST50301 Gall bladder I Homo sapiens CDNA 5' end similar to EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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/clone_lib="dall bladder!"
/note="Organ: gall bladder!" Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: Xho!"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fuldner, R.A.,
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14.3%; Score 100; DB 1; Length 307;
Best Local Similarity 80.6%; Pred. No. 9.4e-08;
Matches 129; Conservative 0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
276 TGTATACATGTGCCATGCTGGTGCTGCACCCACTAACTC 316
                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae; Homo.
1 (bases 1 to 307)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="ATCC" (inhost):145948"
/db_xref="taxon:9606"
/sex="female"
                                                                                                                                                                                                             containing L1 repeat, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Other_ESTs: THC145780
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                 AA344409.1 GI:1996648
                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 3018699423
                                                                                                                                                                                                                                           AA344409
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Volik,S.V., Raphael,B.J., Huang,G.-Q., Murnane,J., Brebner,J.H.,
Valik,S.V., Raphael,B.J., Huang,G.-Q., Murnane,J., Brebner,J.H.,
Bajsarowicz,K., Paris,P., Tao,Q., Kowbel,D., Lapuk,A.V., Kuo,W.-L.,
Shagin,D.A., Shagina,I.A., Magrane,G., Gray,J.W., Jan,F.-C., de
Jong,P., Pevzner,P. and Collins,C.
Decoding the genomic architecture and high throughput detection of
fusion transcripts in breast cancer cell lines: implications for a
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                                                                                                                                   352 recreaectraadaacritaarararararriteriritriterritriarritararrita 411
                                                                                                  216 ATTTTTATTATATACTTTAAGTTTTAGGGTACATGTGCACATTGCGCAGGTTACATA 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
        61
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                MCF731m05TF Human MCF7 breast cancer cell line library (MCF7 1)
Homo sapiens genomic clone MCF7_31m05, genomic survey sequence.
2 TGTTTCACATAAAGTTTTTTTTTTTTGATGATTTTAAAAATATCATTTTCTTTTTTT
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14.3%; Score 100.2; DB 13; Length 870;
Best Local Similarity 76.4%; Pred. No. 8.2e-08;
Matches 123; Conservative 0; Mismatches 38; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UCSF Comprehensive Cancer Center UCSF Box 0808, San Francisco, CA 94143-0808, USA Tel: 415 502 7066 Fax: 415 502 5665
                                                                                                                                                                                                                                         122 ATATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTCA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TATATACATGTGCCATGCTGGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: svolik@cc.ucsf.edu
This clone is available from Amplicon Express
                                                                                                                                                                                                                                                                                                                                                                                                  DNA
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/db_xref="taxon:9606"
/clone="MCF7_31m05"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                             870 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.genomex.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumor genome project
Unpublished (2005)
Contact: Volik SV
Colin Collins' lab
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6/2 bp DNA linear GSS 20-APR-1999
genomic survey sequence.
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Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
Unpublished (1998)
Other_GSSS: RPCIII-53B4.TK
                                   229 ATCCATAAATTTGAAAAAAGTTTAACTACTCTGATAAAAAAGTTTTATAGTTTTCCTACT 288
                                                                                                                                                                                                                                                                                                                                      196 araaaraakgacrecerreraaagriarrirgaagrirelaaaracareaaararreaga 137
   GTTAGTTACATATATATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTCACATGAA 168
                                                                                                                                                                                                    315 CATITITIT - TATTATACTITATGCAAATTAAATTAACTGGCAATCCATTICTTTGCTA 257
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieters@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
class: BAC ends.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                            TTTAAGCAAAATTCCATAGGCCATGGTAATTGTAGTTTCAACATTACTTGCAGTTTCAGT
                                                                                                                                     169 GTTTTTTTAAATTTTAGTGACAGTTTTAGTCATTTTCCTAATTGAAAGTATCATAAGTA
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Pred. No. 9e-08;
0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
The 301 Wedical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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/clone_lib="RPCI-11"
/note="Vector: pBACG3 6, Site_1:
RPCIII Human Male BAC Library"
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/organism="Homo sapiens"
/organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="dD8:7519995"
/db_xref="taxon:9606"
/clone="RPCI-11-5384"
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59.6%;
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Homo sapiens
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Best Local Similarity 59.6
Matches 186; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            289
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1 (bases 1 to 621)

8 Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I.; Scearce,M., Brestli,J., Gradwohl,G. Clifton,S., Hillier,L., Marra,M., Pape,D., While,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Milliams,T., Jackson,Y. and Bowers,Y.

Bndocrine Pancreas Consortium

Unpublished (2000)

Other ESTs: isloal2.xl

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
                                                                                                                                                                                                                                                                                                                                      CA947015 621 bp mRNA linear EST 31-DEC-2002 isl0a12.yl HR85 islet Homo sapiens cDNA clone IMAGE:6364319 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        435 TTTTATTTTTTTTTTTTTTATTATTATACTTTTTAGGGTACATGTGCACACATGTGCAG 376
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Email: dmetcon@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
asshington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
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59.6%; Pred. No. 9.1e-08;
ive 0; Mismatches 125; Indels
                                                                                                     122 ATATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                            121 GTATACATGTGCCATGCTAGTGTGCTGCACCCATTAACTC 82
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Seq primer: -dUDF from Gibco
High quality sequence stop: 481.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA947015.1 GI:27439892
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Homo sapiens
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Fax: 617-495-8557
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CA947015/c
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Hominidae; Homo.

Is Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Barry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building of human bac RPCII1-7542.TJ Contact: Mark Adams

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                         GSS 27-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mdadams@rigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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/clone_lib="RPC1-11"
/note="Vector: pBAce3.6; Site_1: EcoR1; Site_2: EcoR1;
RPCII1 Human Male BAC Library"
                                                                                                     RPCI11-75A2.TK RPCI-11 Homo sapiens genomic clone RPCI-11-75A2
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                         Indels
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      Pred. No. 9e-08;
0; Mismatches 30;
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/mol_type="genomic DNA"
/db_xref="GDB:7528417"
                                                                                                                                                                                                                                                                                                                                                                       272 bp
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/clone="RPCI-11-75A2"
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    ilarity 80.6%;
Conservative
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                       129;
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    Best Local
Matches 12
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677 bp mRNA linear EST 04-SEP-2003
DKF2p313M126_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
DKF2p313M126_5', mRNA sequence.
  TTTTCTTTTTTTATTATTATTATATACTTTTAAGTTTTTAGGGTACATGTGCAAAGTGTGCAG 108
                     168
                                                                                                     228
                                                                                                                                                                                                  328 CATITITIT-TATTATACTITIATGCAAATTAAATTIAACTGGCAATCCATTTCTTTGCTA 386
                                                                                                                                                                                                                                            229 ATCCATAAATTTGAAAAAATGTTAACTACTCCTGATAAAAAAGTTTTATAGTTTTCCTACT 288
                                                                                                                                                                                                                                                                                    387 TCTTTCCCAATICCGGTGTTTCTCAAGITTTTTAAATTTTTGTCTTCCACTAATAGATA 446
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1 (bases 1 to 677)
Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKE2); Email s.wiemannd@kfz- heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the CDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hlcc2)"
Site_1: SfiIA; Site_2: SfiIB;
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This clone (DKFZp313M126) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            289 ITTAAGCAAAATTCCATAGGGCATGGTAATTGTAGTTTCAACATTACTTGCAGTTTCAGT
                                                                                                                                                                                                                                                                                                                                               GTTAGTTACATATATATACATGTGCCATGCTGTGTGTGCTGCACCCATTAACTCACATGAA
                                                                                                                                                            169 GTTTTTTTAAATTTTAGTGACAGTTTTAGTCATTTTCCTAATTGAAAGTATCATAAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wiemann, S.
S. (Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R., et al.)
Unpublished (2003)
On Aug 10, 2001 this sequence version replaced gi:15165163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="313 (synonym:
/note="Vector: pTrip1Ex2;
cDNA-collection"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL601657.2 GI:34476508
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                                                                                                                                                                                                                                                                                                                                                                                                        349 TAGTAAATAAAT 360
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49
                                        208
                                                                                109
                                                                                                                      268
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14.3%; Score 100; DB 1; Length 677;

Query Match

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Hominidae; Homo.
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KEYWORDS
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DA502536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
Direct Submitssion
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail:redgtone@mail.kribb.re.kr, VIR:http://phs.grc.kribb.re.kr/,
Tel:82-42-866-7181, Fax.82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
PRIMERS
                                                                                                                                                                             AG189910 352 bp DNA linear GSS 06-MAR-2004
Pan troglodytes DNA, clone: RP43-064003.T7, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 AGTITITAGGGTACATGTGCACAATGTGCATGTTAGTTACATATGTATACATGTGCCATG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77
                                                                                                                                                                                                                                                                                                     Pan troglodytes
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H. BAC end sequences of Library RP-43 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.2%; Score 99.4; DB 14; Length 352; llarity 84.8%; Pred. No. 1.2e-07; Conservative 0; Mismatches 21; Indels 1
                                                                          201 ATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 238
                                                     124 ATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .352
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RP43-064003.T7"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGTGTGCTGCACCCATTAACTCA 260
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                                                                                                                                                                                                                                                                                     Pan troglodytes (chimpanzee)
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R.Site 1 : EcoRI
R.Site 2 : EcoRI.
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Best Local Similarity
Matches 123; Conserv
                                                                                                                                                                                                                                    AG189910
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ORGANISM
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JOURNAL
REFERENCE
                                                                                                                                           RESULT 32
AG189910
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AUTHORS
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RESULT 33

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FOLITY GRIS TPB RPCI-11 Homo sapiens genomic clone RPCI-11-20K18, B92240.1 GI:2971351
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NBDO human CDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
DAS02536 DAS02536 FCBBF3 Homo sapiens cDNA clone FCBBF3017123 5', mRNA
                                                                                                                                                                                                                                                                                                                                        Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Wakaguri, H., Ishii, S., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yoneyama, T., Otauka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Takahashi-Fujii, A., Takahashi-Fujii, A., Takahashi-Fujii, A., Takahashi-Fujii, A., Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88
                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
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14.2%; Score 99.4; DB 9;
Best Local Similarity 77.1%; Pred. No. 1.2e-07;
Matches 121; Conservative 0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/do xxef="texon:9606"
/db xxef="texon:9606"
/clone="FCBBF3017123"
/tissue_type="brain"
/dev stage="fetal"
/clone lib="FCBBF3"
/note="Vector: pME18SFL3"

    .505
    /organism="Homo sapiens"

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Genome Res. 16 (1), 55-65 (2006)
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                                                                                     DA502536
DA502536.1 GI:80539325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Takao Isogai
                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                   (bases 1 to 505)
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VERSION
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the In.A.G.E. Consortium/LNLL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 2-54, >(TAAA)n#Simple_repeat (matched compliment) 57-287,
>LIPRAZ#LINE/LI (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /done libs-NCI CAPP EIO.
//done libs-NCI CAPP EIO.
//done libs-NCI CAPP EIO.
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//done libs-NCI CAPP EIO.
//done libs a collaboration the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soarse, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-pac vector. The oligonucleotide used to prime the synthesis of first strand cDNA contains a library tag sequence that is located between the Not I site and the (dT1)8 tail. The sequence tag for this library is ACACTIGCAC.
TAG_LISSUE-chondrosarcoma
TAG_LIS-H-EIO
TAG_SEQ-ACACTIGCAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 TTAAGTTCTAGGGTACATATGCACATGCAGGTTTGTTACATATGTATACATGTGCCA 126
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     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
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/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 99.4; DB 3;
Pred. No. 1.1e-07;
0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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/clone="IMAGE:5838669"
/tissue_type="Chondrosarcoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 TGCTGGTGTGCTGCACCCATTAACT 160
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84.8%;
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Homo sapiens
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Best Local Similarity
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BQ924499/c
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                                                                                                           Adminidae; Homo.

18 (bases 1 to 549)

Adams, W. D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.

Use of BAC End Sequences for Sequence-Ready Map Building (1998)

Unpublished (1998)

Other_GSS: RPCIII-20K18.TV

Contact: Mark Adams

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208

Fax: 301 838 0208

Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-II. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (inf@resgen.com). BAC end search/bac_end_search.html
Seg primer: SP6
Seg primer: SP6
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UI-H-EIO-ayh-c-22-0-UI.S1 NCI_CGAP_EIO Homo sapiens cDNA clone
IMAGE:5838669 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 TTATTATACTITITAAGTITITAGGGTACATGTGCAAAGTGTGCAGGTTAGTTACATATATA 124
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="Lymphocytes"
/clone lib="RPC1-11"
//note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 TACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .548
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic_DNA"
/db_xref="GDB:7507553"
/db_xref="taxon:9606"
/clone="RPCI-11-20K18"
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BQ007697.1 GI:19732597
                         sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sex="Male
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1 (bases 1 to 771)
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                                                   sapiens
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Matches 121; Conserv
                            Homo
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KEYWORDS
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AUTHORS
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BQ007697
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                                                                                                                                                                                                                                                       library availability please contact Pieter de Jong Pipters/deejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html class: BAC ends.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. While, T. project 1997
Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA446110

401 bp mRNA linear EST 03-JUN-1
Zw60b03.s1 Soares total fetus NB2HP8-9w Homo sapiens CDNA clone
IMAGE:774413 3' similar to 9b:i19872 AH RECEPTOR PRECURSOR
(HUMAN);contains L1.b2 L1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPGI-11"
/note="Vector: pBAcB.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
Other_GSSs RPCIII-10717.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Enkaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
Examil: hbedeigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365 GGTGTGCTGCACCCATTAACTCTTTAGCATTAGGTATATCT 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 GGTGTGCTGCACCCATTAACTCACATGAAGTTTTTTTAAATTT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 99.2; DB 11;
Pred. No. 1.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic_DNA"
/db_xref="GDB:7540902"
/db_xref="taxon:9606"
/clone="RPCI-11-10717"
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79.3%;
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AUTHORS
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JOURNAL
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AA446110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="Lupski sciatic nerve"
/note="Vector: pGWV-SPORT6 (Life Technologies); Site_1:
Not1; Site_2: Sal1; DNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACTAGTTCTAGATCGCGGCGCCCCCT(IS)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUJ19769 571 bp DNA linear GSS 06-MAY-1999 RPCI11-10717.TV RPCI-11 Homo sapiens genomic clone RPCI-11-10717, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148
                                                                                                                                                         Email: cgapbe_remail.hth.gov
Tissue Procurement: Dr. James R. Lupski
DNN Albrary Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM13608 row: p column: 09
High quality sequence stop: 554.
Localion(Qualifiers

1. 906
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I (bases 1 to S71)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae, Homo.

1 (bases 1 to 906)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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0
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Pred. No. 1.1e-07;
0; Mismatches 36; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 ACATGTGCCATGCTGGTGCTGCACCCATTAACTCA 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
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ilarity 77.1%;
Conservative
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Best Local Similarity
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AQ319769
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AUTHORS
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Kinura, Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yawamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishidi, S., Sugiyama, T., Satco, K., Isono, Y., Irie, R., Kuchida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishidashi, Y., Takahashi-Puji, A., Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Genome Res. 16 (1), 55-65 (2006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from sesarch Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                    /cell_type="Lymphocytes"
/clone_lib="RPC1-11"
//note="Vector: pBACB 6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 TTAGGGTACATGTGCACATTGTGCAGGTTAGTTACATATGTATACATGTGCCATGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITITGATGATTATAATAAAAATATCATTITTTTTTTTTATTATTATAATAAGTT
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DB302517 BRAMY2 Homo sapiens cDNA clone BRAMY2030702 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 99; DB 11; Length 46
Pred. No. 1.4e-07;
0; Mismatches 25; Indels
                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                              /mol_type="genomic_DNA"
/db_xref="GDB:7515691"
/db_xref="taxon:9606"
/clone="RPCI-11-41N20"
                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 GTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 GCGCTGCACCACTAACTC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: flj-cdna@nifty.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB302517.1 GI:83085415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.1%;
82.0%;
                                                                                                                                                                                                                                                                                                                                  /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114; Conservative
                                                                                                                                                                          1. .464
                                                                                                                              Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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Best Local 9
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DB302517/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ029723 464 bp DNA linear GSS 14-APR-1999
RPCIl1-41N20.TV RPCI-11 Homo sapiens genomic clone RPCI-11-41N20,
                                                                                                                                                                                                                                                                                                                                                                                                     Eco RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 464)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and
Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 TITITITICATGATTITAATAAAATATCATTITCTTTTTTTTATTATTATAACTTTTAAG 80
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 314 286 1810
Bmail: est@waston.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -47n13 fwd. ET from Amersham
High quality sequence stop: 369.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of BAC End Sequences for Sequence-Ready Map Building (1998)
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Soares total_fetus_Nb2HF8_9w"
/note="Vector: pT773D-PaCi; Site_l: Not I; Site_2: Ex
Is strand CDNA was prepared from mRNA obtained from
pooled 8-9 week (total) fetus material with a Not I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.1%; Score 99; DB 1; Length 401; 86.5%; Pred. No. 1.4e-07;
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): Mismatches 15; Indels
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                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                        /dev_stage="8-9 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                 clone="IMAGE:774413"
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AQ029723.1 GI:3274854
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Homo sapiens
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Matches 122; Conserv
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Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
Center, National Institute of Technology and Evaluation; 3'-end one
                                                                                                                                                                                                                                                                      ı,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS 01-NOV-2001
                                                                                                                                                                                                                                                                                                                                              79 AGTTTTAGGGTACATGTGCAAAGTGTGCAGGTTAGTTACATATATACATGTGCCATGC 138
                                                                                                                                                                                                                                                                                                                                                                                                   AG042325 665 bp DNA linear GSS 01-NOV-200
Pan troglodytes DNA, clone: PTB-020E21.F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                          78
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                          Gaps
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fuliyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                  14.1%; Score 99; DB 9; Length 553; 85.3%; Pred. No. 1.4e-07; ive 0; Mismatches 20; Indels
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-020E21.F"
                                                                  /organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="BRAMX2030702"

/tissue_type="amygdala"

/clone_lib="BRAMX2"
                                                                                                                                                                             /note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell_type="lymphoblast"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGTGTGCTGCACCCATTAACTC 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 TGGTGTGCTGCACCCATTAACTC 161
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                pass sequencing: RAB.
Location/Qualifiers
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R.Site 1 : SacI
R.Site 2 : SacI.
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                                                                                                                                                                                                                                                     Best Local Similarity
Matches 122; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           399
                                                                                                                                                                                                                                    Query Match
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AUTHORS
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AG042325
LOCUS
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High Throughput Sequencing Center
High Throughput Sequencing Center
High Throughput Sequencing Center
University of Mashington
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Tel: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derivved from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu). Clones way be purchased from
Clones are Agenetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1147 row: P column: 20
Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae; Homo.

1 (bases 1 to 704)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Kellar, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSS 02-AUG-1999
                                                                                                                                                                                                                                                        79 AGTTTTAGGGTACATGTGCAAAGTGTGCAGGTTAGTTACATATATACATGTGCCATGC 138
                                                                                                                                                                                                                                                                                                                                                                                            353 AGTTTTAGGGTACATGTGCACAATGTGCAGGTTAGTTACCTATGTATACATGTGCCATGC 412
                                                                                                                                                                                                                  78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ779743 1inear GSS 02-AUG-
HS_5571_B2_H10_SP6_RPCI-11 Human Male BAC_Library Homo sapiens
genomic_clone Plate=1147 Col=20 Row=P, genomic_survey sequence.
                                                                                                                                                                                                                  19 TITITITITIGATGATTITAATAAAATATCATTITITTTTTTTTATTATTATAATATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                      Gaps
                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                           Length 665;
                                                                                                                                                      20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol type="qenomic DNA"
/db xref="taxon:9606"
/clone="Plate=1147 Col=20 Row=P"
                                                                                           DB 14;
1.4e-07;
                                                                                           Score 99; DB
Pred. No. 1.4e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 704.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                413 TGGTGCGCTGCACCCACTAACTC 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 TGGTGTGCTGCACCCATTAACTC 161
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                                                                                           14.1%;
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                                                                                                                                                      122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .704
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Hominidae, Homo.

1 (Dases I to 424)

Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Building (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ127855 13-SEP-1998 HS_3094_A1_B02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3094 Col=3 Row=C, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae, Homo.
1 (Dases I to 468)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                               Unpublished (1998)
Other GSSs: CIT-HSP-2328018.TF
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: Ml3 Reverse
Class: BAC ends.
                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.1%; Score 98.8; DB 11; Length 424; 79.6%; Pred. No. 1.5e-07; ive 0; Mismatches 32; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTATACATGTGCCATGCTGTTGTGTTGTGTGTAACTCA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TATATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTCA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="2328018"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                      sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 129; Conservative
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AQ127855.1
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                    SOURCE
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AQ042547.1 GI:3309932
                                                                                                                                                                                                                                                                                                                                                                           EST 08-SEP-1994
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                                                                                                                                                  44 TATCATTTTCTTTTTTTATTATTATATACTTTTAAGTTTTTAGGGTACATGTGCAAAGTG 103
                                                                               70
                                                                                                                 17
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(bases 1 to 419)

(bases 1 to 419)

(bases 2 to 419)

(bases 3 to 419)

(c) Behar, G., Bois, F., Bouchier, C., da Silva, C.,

(c) Behar, S., Houlgatte, R., Jumeau, M.N., Lamy, B.,

(c) Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y.,

Sebastiani-Kabaktchis, C. and Tessier, A.

IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 TGCAGGTTAGTTACATATATATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z36956
HHEA81M Atrium CDNA library Human heart Homo sapiens CDNA clone
HEA81M, mRNA sequence.
                                                                                                 Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and its expression
C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
7757816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Atrium cDNA library Human heart
Score 99; DB 11; Length 704;
                                        25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratorium fuer molekulare Biologie
Am Klopferspitz 18a,8033 Martinsried,Germany
Email: obermaier@vms.biochem.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.1%; Score 98.8; DB 10;
89.8%; Pred. No. 1.5e-07;
ative 0; Mismatches 12;
                  Pred. No. 1.4e-07;
0; Mismatches 25
                                                                                                                                                                                                                                                         137 TICCATGCTGGTGTGCTGCACCCATTAACTC 167
                                                                                                                                                                                                                                 131 TGCCATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEA81M"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Genzentrum Muenchen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
14.1%;
82.8%;
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EST.
                                    Matches 125; Conservative
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Best Local Similarity
Matches 106; Conserv
                  Similarity
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Query Match
                      Best Local
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Venter, J.C.

Venter, J.C.

Was Building

Building

L. Unpublished (1997)

Other_GSS: RPCI-11-383F14.TJ

Conteact: Shaying Zhao, William Nierman, Mark Adams

Conteact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0208

Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS 28-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 ATACTITAAGTITITAGGGTACATGTGCAAATGTGCAGGTTAGTTACATATGTACATG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae, Homo.
1 (bases 1 to 561)
Zhoo.S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.
                                                                                 Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3094 row: C column: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 98.8; DB 11; Length 468; Pred. No. 1.5e-07; 0; Mismatches 32; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ550918 1inear GRPCI-11-383F14.TV RPCI-11 Homo sapiens genomic clone RPCI-11-383F14, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="Plate=3094 Col=3 Row=C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 TGACATGCTGGTGCGCTGCACCACTAACT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 TGCCATGCTGGTGTGCTGCACCCATTAACT 160
                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                      High quality sequence stop: 468.
Location/Qualifiers
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AQ550918.1 GI:4910095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 78.7%;
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                           . .468
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                             source
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VERSION
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AUTHORS
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COMMENT
                                                                       PUBMED
                                              JOURNAL
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          TITLE
                                                                                       COMMENT
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. M. Benco Soares, University of Iowa
CDNA Library preparation: Dr. M. Benco Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Benco Soares, University of Iowa
DNA Sequencing by: Dr. M. Benco Soares, University of Iowa
DNA Sequencing by: Dr. M. Benco Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-48, > (TAAA) n#Simple repeat (matched compliment) 51-169,
>LIPA2#LINE/L1 (matched compliment) 413-454,
>AT rich#Low complexity 498-590, >MIR#SINE/MIR (matched compliment)
Seq primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BQ447264 1-23-0-UI.sl NCI CGAP Ctl Homo sapiens CDNA clone UI-H-EU1-bad-1-23-0-UI.s', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                479 Triragcongretaterinininerininarininarininarinarinarinarinin 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                library availability, please contact Pieter de Jong pieter@dejong.med.buffalo.edu. Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.seq primer: T7 class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Homoinidae; Homo.

1 (Dases 1 to 725)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP); Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="Lymphocytes"
/clone lib="RFCI-11"
/note="Vector: pBACe3.6; Site_1: EcoR1; Site_2: EcoR1;
RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 ATACATGTGCCATGCTGGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 98.8; DB 11;
Pred. No. 1.5e-07;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                  Location/Qualifiers
1. .561
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                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/db_xref="GDB:7646821"
/db_xref="taxon:9606"
/clone="RPCI-11-383F14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cocation/Qualifiers
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BQ447264.1 GI:21250376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 76.6%;
Matches 121; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens
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1; Gaps

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169

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Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Neb site: http://www.nisc.nih.gov/
Contact: nisc_mgcompgri.nih.gov/
Shther,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Grannite,S., Guan,X., Gupta,J., Haghighi,P.,
Blansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                    //ncte="Vector: pBCBAC1; Site 1: HindIII; This library was
constructed from MCF7 breast cancer cell line by Amplicon
Express (http://www.genomex.com) using their standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 3088)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                   /clone lib="Human MCF7 breast cancer cell line library
(MCF7 1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 TITATITITIATITITITATITITITATITITITIAAAITITITITITITITATITITATITATIATAAATIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 98.8; DB 13;
Pred. No. 1.5e-07;
0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3088 bp mRNA
Homo sapiens, clone IMAGE:5210997, mRNA.
BC032464
                                                                                   1. .853
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 TGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 TGCTGGTGCGCTGCACCCATTAAGTC 84
                                                                                                                                    /mol_type="genomic_DNi
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/clone="MCF7_25h15"
/sex="female"
                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BC032464.1 GI:22749645
  http://www.genomex.com
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.1%;
84.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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Best Local S
                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 49
BC032464/c
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
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JOURNAL
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                                                          FEATURES
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                                         /Lione=Will-Exclusions
/Lione=Will-Exclusions
/Lissue type="Osteoarthritic Cartilage"
/Lissue type="Osteoarthritic Cartilage"
/Lissue type="Osteoarthritic Cartilage"
/Lissue type="Osteoarthritic Cartilage"
/Lione lib="NOI CGAP Ctl"
/Lione lib="NOI CGAP Ctl"
/Lione lib="NOI CGAP Ctl"
/Lione lib="NOI CGAP Ctl"
/Lione lib="NOI CGAP Ctl"
/Lione lib="NOI CGAP Ctl"
/Lione lib="NOI Is a normalized cDNA library containing the following tissue(s): Osteoarthritic Cartilage The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996 First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT/TJ-pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae; Homo.

1 (bases 1 to 853)
Volik,S.V., Raphaei,B.J., Huang,G.-Q., Murnane,J., Brebner,J.H.,
Bajsarowicz,K., Paris,P., Tao,Q., Kowbel,D., Lapuk,A.V., Kuo,W.-L.,
Bajsarowicz,K., Paris,P., Tao,Q., Kowbel,D., Lapuk,A.V., Kuo,W.-L.,
Shagin,D.A., Shagina,I.A., Magrane,G., Gray,J.W., Jan,F.-C., de
Jong,P., Pevzner,P. and Collins,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CZ446241 GSS 20-OCT-2005 MCF725h15TF Human MCF7 breast cancer cell line library (MCF7_1) Homo sapiens genomic clone MCF7_25h15, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Decoding the genomic architecture and high throughput detection of fusion transcripts in breast cancer cell lines: implications for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ritritritritritritricaagacircritairratritairiaritairatratrac-r 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 TITITITITITICATGATTTTAATAAATATCATTTTCTTTTTTTTTATTATACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (dT)18 tail. The sequence tag for this library is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UCSF Comprehensive Cancer Center UCSF Box 0808, San Francisco, CA 94143-0808, USA Tel: 415 502 7066 Fax: 415 502 5665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: svolik@cc.ucsf.edu
This clone is available from Amplicon Express
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAG TISSUE-osteoarthritic cartilage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 98.8; DB 3
Pred. No. 1.5e-07
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 TGCTGGTGTGCTGCACCACTAACTC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCTGGTGTGCTGCACCCATTAACTC 161
                           xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAG_LIB=UI-H-EU1
TAG_SEQ=TGATCACGCT"
'mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CZ446241.1 GI:77922503
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84.2%;
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Unpublished (2005)
Contact: Volik SV
Colin Collins' lab
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Best Local (
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CZ446241/c
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1. (bases 1 to 324)

3. Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Uge of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

1. Unpublished (1998)

2. Other GSSs: CIT-HSP-2304A13.TF

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research

7.12 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 64 Row: j Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3004 TTAAGTICTAGGGTACATGTGCACAACGTGCAGGTTAGTTACATATGTATACATGTGCCA 2945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS 09-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
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Momo sapiens
Eukaryots, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 bp DNA linear GSS 09-JUN CIT-HSP-2104A13.TR CIT-HSP Homo sapiens genomic clone 2304A13, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Length 3088;
                                                                                                      analysis
This clone has the following problem: frame shifted.
                                                                                                                                        Location/Qualifiers
1. 3088
1. 3088
1. 4008="mRNA"
| Mol_type="mRNA"
| Lype="traxon,9606"
| Clone="INAGE:510997"
| Clone="ID="NHAGE:118"
| Clone="D="NHAGE:118"
| Clone="D="NHAGE:109"
| Clone="D="NHAGE:109"
| Clone="NHAGE:100"
| Clone="NHAGE:100"
| Clone="NHAGE:100"
                                                                                                                                                                                                                                                                                                                                                                                                                            22; Indels
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
14.1%; Score 98.8; DB 6;
Best Local Similarity 84.2%; Pred. No. 1.4e-07;
Matches 123; Conservative 0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2944 TGTTGGTGTGCACCCATTAACTC 2919
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 TGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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AQ017761.1 GI:3196497
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AQ017761
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AUTHORS
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COMMENT
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Hominidae; Homo.
1 (bases 1 to 398)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Mahairas,G.G., Wallace,J.C., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ605001
HS 2119_B1_A12_T7C CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2119 Col=23 Row=B, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                72 ACTITIAAGITITIAGGGIACAIGIGCAAAGIGIGCAGGITAGITACAIATATATATACAIGI 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High Throughput Sequencing Center University of Washington University of Washington Of Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3887 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Elmail: jwallace@u.washington.edu Elmail: jwallace@u.washington.edu PakC end Web Server: http://www.htsc.washington.edu Plate: 2119 row: B column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                   /cell_type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
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                                                                                                                                                                                                                                 14.1%; Score 98.4; DB 11; Length 324; 79.1%; Pred. No. 1.8e-07; ive 0; Mismatches 31; Indels 0.
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/organism="Homo sapiens"
/orl_type="genomic DNA"
/db_xref="texcn:9606"
/clone="Plate=2119 Col=23 Row=B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 GCCATGCTGTGCTGTACCCACTAAC 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 GCCATGCTGGTGTGCTGCACCCATTAAC 159
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High quality sequence stop: 398.
Location/Qualifiers
/db_xref="taxon:9606"
/clone="2304A13"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
AQ605001
AQ605001.1 GI:5064995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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10-661966-1 146001-146700 a146311.rst

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EST 21-FEB-2003

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/organism="Homo sapiens"

/mol type="mRNR"

/db_xref="taxon:9606"

/db_xref="taxon:9606"

/clone="UTCF=RNO-aeu-e-07-0-UI"

/tissue type="Human Lung Epithelial cells"

/lab_host="BHIOB (Life Technologies) (T1 phage resistant)"

/clone lib="HUTCF=RNO"

/clone lib="UTCF=RNO"

/clone lib="taror yout surpray of the amodified polylinker; Site—1: EcoR I; Site—2: Not I;

/u-CF-RNO is a subtracted cDNA library derived from two
normalized Human lung epithelial cell libraries (EN1 and
DU1) The library was subtracted according to according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. For additional information, contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Iowa Tolana Med Labs, Iowa City, IA 52242, USA 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA Tex: 319 356 7171

Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa CLOne Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems

(www.openblosystems.com)
The following repetitive elements were found in this CDNA sequence: 20-114, >LIPR2#LINE/L1 (matched compliment) 116-273, $64 primer: M13 FORWAD
POUXA=Yes.
                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae, Homo, [1] (bases 1 to 273)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                    BU607283
UI-CF-FN0-aeu-e-07-0-UI.S1 UI-CF-FN0 Homo sapiens cDNA clone
UI-CF-FN0-aeu-e-07-0-UI 3', mRNA sequence.
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TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG_LIB=UI-CF-FN0
       Pred. No. 1.7e-07;
0; Mismatches 31; Indels
                                                                                                                                                                                                                                                        121 TATATACATGTGCCATGCTGGTGTGCTGCACCCATTAACT 160
                                                                                                                                                                                                                                                                               335 TGTATACATGTGCCATGCTGGTGCTGCTGCACCATTAAAT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Res. 6 (9), 791-806 (1996)
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  80.08;
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    Best Local Similarity 80.0
Matches 128; Conservative
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BU607283
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S Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.
Radelof, U., Schneider, D. and Korn, B.
Human Uniqeneset - RZPD3
Contact: Ina Rolfs
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGP998MH8117.
RZPDLIB; I.M.G.E. cDNA Clone Collection;
Human Uniqeneset - RZD3 (RZPDLIB No. 972)
http://www.rzpd.de/CloneCards/Cgi-
bin/showLib.pl.cgi/response7libNo-972
bin/showLib.pl.cgi/response7libNo-972
bin/showLib.pl.cgi/response7libNo-972
cl: +49 30 32639 101
www.rzpd.de
www.rzpd.de
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                                                                                                                                                                                                                                                                                                                                                                                                                                   BX115372 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGP998M18117; IMAGE:123065, mRNA sequence.
                                                                                                                    224 TITTAAGITTTTAGGGTACATGTGCACATTGTGCAGGTTAGTTACATATGTATACATGTGC 283
                                                                                             73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seg primer: M13r, Primer sequence: TTTCACACAGGAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                          Gaps
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Score 98.4; DB 11; Length 398; Pred. No. 1.8e-07;
                                               Indels
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/db_xref="taxon:9606"
/clone="IMAGp998M18117 ; IMAGE:123065"
                                                  31;
                                             0; Mismatches
                                                                                                                                                                                                                                                                           134 CATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                  284 CATGCTGGTGCGCTGCACCCACTAACTC 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .713
/organism="Homo sapiens"
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14.18;
79.18;
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                     Best Local Similarity /9.1
Matches 117; Conservative
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  Query Match
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DEFINITION
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BX115372
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14.1%; Score 98.4; DB 4; Length 713;

Query Match

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Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
Tel: 81-438-52-3975
Fax: 81-438-52-3975
Fax: 81-438-52-396
Email: flj-cdna@nifty.com
BEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Murakawa, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification of Transcriptional Modulation: Large-scale Promoters of Human Characterization of Putative Alternative
                                                                                                                                                                                                                                        DB097926 TEST14 Homo sapiens CDNA clone TEST14049307 5', mRNA
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Pred. No. 1.9e-07;
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                                                                                                                                         201
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                                                                                                                      171 TGCCATGCTGGTGTGCTGCACCCATTAACTC
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/clone_lib="TEST14"
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nilarity 83.7%;
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                                                                                                                                           49 TTTTCTTTTTTTATTATTATTATTATTATAGTTTTAGGGTACATGTGCAAAGTGTGCAG 108
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Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
RREBACPA Genet cs (info@resgen.com). BAC end search page:
http://www.ligr.org/td/b/humgen/bac end search/bac end search page:
http://www.ligr.org/td/b/humgen/bac end search/bac end search.html.
This BAC end was generated during the R&D process and may have
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/clone lib="RPC1-11"
/note="Vector: pBACe3.6; Site_1: EcoR1; Site_2: EcoR1;
RPCI11 Human Male BAC Library"
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae; Homo.
1 (bases 1 to 555)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.
                                                                                                                                                                                                                           109 GTTAGTTACATATATATACATGTGCCATGCTGGTGCTGCACCCATTAAC 159
                                                                                                                                                                                                                                                     64 GTTAGTTACCTATGTATACATGTGCCATGCTGGTGTGCTGCACCACTAAC 114
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                                                                                                                                                                                                                                                                                                                                                                               RPCI-11-357P22.TJB RPCI-11 Home sapiens genomic clone NPCI-11-357P22, genomic survey sequence.
                                                           Score 98.2; DB 3; Length 273; Pred. No. 2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 TAAAGTTTTTTTTTTTGATGATTTTAATAAAATATCATTTTCTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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78.1%; Pred. No. 1.9e-07;
iive 0; Mismatches 33;
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Unpublished (1997)
Other_GSSs: RPCI-11-357P22.TV
                                                                                                 0; Mismatches
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1. 555
/organism="Homo sapiens"
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/clone="RPCI-11-357P22"
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/db_xref="GDB:7637085"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                  555 bp
TAG_SEQ=GGCTGTAGGC
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                                                           14.0%;
92.8%;
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                                                                                  Best Local Similation ....
Matches 103; Conservative
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Class: BAC ends.
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es 118; Conserv
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survey sequence
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1 (bases 1 to 226)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: head neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                         8Q352132 220-MAY-2002
IL3-HT0619-100700-208-A10 HT0619 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-HT0619-
100700-208-A10&t3=2000-07-10&t4=1)

Seq primer: puc l8 forward

High quality sequence stop: 226.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shorgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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497 TGCTGGTGTGCTGCACCCATTAACTCA 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0619"
                                                                                                                                                                    BQ352132.1 GI:21016188
                                                                                                                                                                                                               Homo sapiens (human)
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Matches 104; Conservative
                                                                                                                                                                                                                                        Homo sapiens
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AQ628311
                                                            RESULT 56
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Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
                                                                                                                                                                                                                                                                                                                         Map Building
Unpublished (1997)
Other GSSs: CITBL-E1-2650L21.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0200
Fax: 301 838 0200
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
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                                                                                                                                                                                                                                                                                                     Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="sperm"
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/clone="Vector: The CTRB1-B1"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 740)
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Pred. No. 2.1e-07;
0; Mismatches 25; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA"
/db_xref="taxon:9606"
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AQ628311
AQ628311.1 GI:5090703
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82.7%;
                                                                                Homo sapiens (human)
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1 (bases 1 to 480)
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Matches 128; Conservative
               Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                       Class: BAC ends.
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CR750736/c
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Use of BAC End Sequences for Sequence-Ready Map Building Unpublished (1997)
Other GSSs: RPCIII-12116.TV
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                       derived from Pieter J. de Jong library RPCI-3;
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDB737G0315D
RZPDLIB; (Human Genomic Set - RZDD 1.0) RZPD LIB No.737
http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=737
contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Fax: +49 30 32639 100
www.rzpd.de

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                 Submitted (07-JUN-2005) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 515, D-69120 Heidelberg,
                                                                                                                                                                                                                                                                                                              This clone is available from RZPD;
Contact RZPD (customer.service@rzpd.de) for further information.
Clone distribution: http://www.rzpd.de/products/genomicset/
Seq-primer: T7 (TAA-TAC-GAC-TCA-CTA-TAG-GG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="RPCI-3"
/note="Vector: pCYPAC2; RPCI-3 Human Male PAC Library"
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Schwarz, F., Neubert, P., Schneider, D., Peters, M. and Korn, B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 740;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
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/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic_DNA"
/db_xref="taxon:9606"
                                                                        Germany
RZPD; RZPDB737G0315D; RP3-416J7;
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B75832.1 GI:2771519
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les 127; Conserv
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B75832
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CR750736 657 bp mRNA linear EST 30-AUG-2004 DKFZp470L1122 rl 470 (synonym: pliv1) Pongo pygmaeus cDNA clone DKFZp470L1122-5', mRNA sequence.
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                                                                        Email: maddams@ligr.org

Clones are derived from the human BAC library RPCI-11. For BAC

Library availability, please contact Pieter de Jong

(pieter@dejong med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
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Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pongo pygmaeus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 65.7)
Poustka, Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pongo pygmaeus mRNA (Poustka,A., Albert,R., Moosmayer,P., et al.)
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Lymphocytes"
/clone_lib="RPC1-11"
/note="Vector: pBACe3.6; Site_l: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 TITCACATAAAGITITITITITITIGAIGATITITAATAAAATATCATITITITITITITITITI
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Center Dr., Rockville, MD 20850, USA
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Pred. No. 2.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                1. .385
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic_DNA"
/db_xref="GDB:7504431"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="RPCI-11-12116"
                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pongo pygmaeus (orangutan)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CR750736
CR750736.1 GI:51669903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="Male"
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468

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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3868
Fax: (206) 616-3868
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Seq primer: 680 row: B column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae; Homo.
1 (bases I to 513)
Mahaharas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib-"RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                    23-APR-1999
  349 AAAGTTTTCCCACTATTATTTAATTTACATAATATTTTTAATTNTATTATTATTA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                        72 ACTITIAAGITITAGGGTACATGTGCAAAGTGTGCAGGTTAGTTACATATATACATGT
                                                             409 TACTITAAAGTITITAGAGTACATGTGCACAATGTGCAGGTITGNIACATATGTATACATGTT
                                                                                                                                                                                                                                                                  AQ464599 11.00 S13 bp DNA linear GSS 23-APR-HS_5104_B2_A11_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=680 Col=22 Row=B, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.9%; Score 97.6; DB 11; Length 513; 79.9%; Pred. No. 2.4e-07; ive 0; Mismatches 29; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="Plate=680 Col=22 Row=B"
                                                                                                                                               469 GCCATGTTGGTGTGCTGCACCCATCAACTCA 499
                                                                                                                     132 GCCATGCTGGTGTGCTGCACCCATTAACTCA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .513
/organism="Homo sapiens"
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High quality sequence stop: 513.
Location/Qualifiers
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AQ464599.1 GI:4641694
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male
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Matches
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PUBMED
COMMENT
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                                                                                                                                                                                                                           RESULT 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AFI18407 Homo sapiens skin ALU-PCR Homo sapiens genomic clone T2, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                    101
                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="470 (synonym: pliv1)"
/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"
                                                                                                                                                                                                                                                                                                                              94
                                                                                                                                                                                                                                                                                                                                                                                                                                                   41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Cavalli, F.,
                                                                                                                                                                                                                                                                                                                                                                  TITITITITITITICATGATTITAATAAATATCATTITITITITITITATTATAATATTAT
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call_type="ptimer"
foal_type="ptimer"
/clone lib="Homo sapiens skin ALU-PCR"
/note="ALU-PCR fragment obtained with ALU4 primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                             Length 657;
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1 (Dases 1 to 724)

Bertoni,F., Mullenbach,R., Broggini,M., Roggero,E., (Cotter,F. and Zucca,E.
Extranodal marginal zone B-cell lymphoma genotyping lAlu-polymerase chain reaction
10953982
                                                                                                                                                                                                                                                                                     22; Indels
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Istituto di Ricerche Farmacologiche 'Mario Negri'
via Britrea 62, Milan, 20157, Italy
absent in matched peripheral blood
                                                                                                                                                                                                                                          Score 97.8; DB 8;
Pred. No. 2.2e-07;
0; Mismatches 22;
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0; Mismatches 34
                   /organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA'
/db_xref="taxon:9606"
                                                                               /clone="DKFZp470L1122"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 GCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="liver"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: Alu-PCR.
Location/Qualifiers
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                                                                                                                                                                                                                                             14.0%;
84.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Bertoni F
                                                                                                                                                                                                                                                              Best Local Similarity 84.13
Matches 122, Conservative
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AF118407
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                                                                                                                                                                         CZ465237 108 bp DNA linear GSS 20-OCT-2005 MCF756k05TF Human MCF7 breast cancer cell line library (MCF7_1) Homo sapiens genomic clone MCF7_56k05, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                  Hominidae, Homo.

1 (Bases I to 708)

1 (Bases I to 708)

Sarowicz, K., Paris, P., Tao, Q., Kowbel, D., Lapuk, A.V., Kuo, W.-L., Shagin, D.A., Shagina, I.A., Magrane, G., Gray, J.W., Jan, F.-C., de Jong, P., Pevzner, P. and Collins, C.

Decoding the genomic architecture and high throughput detection of fusion transcripts in breast cancer cell lines: implications for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pECBAC1; Site_1: HindIII; This library was constructed from MCF7 breast_cancer cell line by Amplicon Express (http://www.genomex.com) using their standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 ATACTTTTAAGTTTTTAGGGTACATGTGCCAAAGTGTGCCAGGTTACTTATATACAT 129
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumor genome project
Unpublished (2005)
Contact: Volik SV
Colin Collins' lab
UCSF Comprehensive Cancer Center
UCSF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 502 7066
Fax: 415 502 5665
Email: svolik@cc.ucsf.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: svolik@cc.ucsf.edu
This clone is available from Amplicon Express
http://www.genomex.com
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 GTGCCATGCTGGTGCGCTGCACCACTAACTC 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="MCF7_56k05"
/sex="female"
                                                   136 TGCTGGTGTGCTGCACCCATTAAC 159
                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                 CZ465237.1 GI:77948426
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                                                                                                                                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
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tes 118; Conserva
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AUTHORS
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COMMENT
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CZ465237
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SOURCE
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64

RESULT

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E 1 (bases 1 to 443)
S Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and
Venter, J.G.
Use of BAC End Sequences for Sequence-Ready Map Building
Unpublished (1997)
Unpublished (1997)
Unpublished End Sequences for Sequence-Ready Map Building
Context. Mark Adams
Department of Edvaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fan troglodytes DNA, clone: PTB-130G10.F, genomic survey sequence. AG121371. G1:16650536 GSS.
Pan troglodytes (chimpanzee)
B72013 443 bp DNA linear GSS 08-APR-1999 RPCIII-7E20.TV RPCI-11 Homo sapiens genomic clone RPCI-11-7E20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              o;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Seq primer: T7
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="Lymphocytes"
/clone lib="RPC1-11"
/note="Vector: pBAce3.6; Site_1: EcoR1; Site_2: EcoR1;
RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 TITITITITITITIGAIGALTITIAATAAATAICATITITITITITITIATTATTATACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.9%; Score 97.4; DB 11; Length 443; 78.9%; Pred. No. 2.7e-07; ive 0; Mismatches 31; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 TGCTGGTGTGCTGCACCCATTAACTCA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         380 TGCTGGTGCGCTGCACCCACTATCTCA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA"
/db_xref="GDB:7502419"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="RPCI-11-7E20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                         genomic survey sequence.
                                                                                                       B72013.1 GI:2711234
                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 78.9
Matches 116; Conservative
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                                                                                                                                                                                         Homo sapiens
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ACCESSION
VERSION
KEYWORDS
SOURCE
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Carter, J., Cordes, M., Harris, A., Isak, A., van Brunt, A., Nguyen, C., Du, F., Courtney, L., Kalicki, J., Ozersky, P., Abbott, S., Armstrong, J., Belter, E.A., Caruso, L., Cedroni, M., Cotton, M., Davidson, T., Desai, A., Elliott, G., Erb, T., Fronick, C., Gaige, T., Haakenson, W., Haglund, K., Holmes, A., Harkins, R., Kim, K., Kruchowski, S.S., Strong, C.M., Grewal, N., Goyea, E., Hou, S., Levy, A., Martinka, S., Mead, K., McLellan, M.D., Meyer, R., Randall-Maher, J., Goninson, C., Dauphin-Kohlberg, S. et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   End-sequence profiling: Sequence-based analysis of aberrant genomes Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003) 12788976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BZ610242 1near GSS 08-JUN-2003 WHADR41TF Human MCF7 breast cancer cell line library (MCF7_1) Homo sapiens genomic clone MCF7_1-23G10, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Vollk, S., Zhao, S., Chin, K., Brebner, J.H., Herndon, D.R., Tao, Q.,
Kowbel, D., Huang, G., Lapuk, A., Kuo, W.-L., Magrane, G., de Jong, P.,
Gray, J.W. and Collins, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.9%; Score 97.4; DB 13; Length 712; Best Local Similarity 78.9%; Pred. No. 2.6e-07; Matches 116; Conservative 0; Mismatches 31; Indels 0.
                                                                                                                                                                                                                                                                                                                                                  63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UCSF Comprehensive Cancer Center UCSF Box 0808, San Francisco, CA 94143-0808, I Tel: 415 502 7066 Fax: 415 502 565 Fax: 11 501 502 565 Faxil: svolik@cc.ucsf.edu This clone is available from Amplicon Express
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA"
/db_xref="taxon:9598"
/clone_lib="Chimpanzee genomic_DNA"
                                                                                                                                                                                                                                                                                                   Genome Sequencing Center
Washington University School of Medicine
4444 Forest Park Parkway, St. Louis, MO (
                                                                                                                                                                                                                                                                                                                                                              Tel: (314)266-1839
Fax: (314)286-1810
Email: submissions@atson.wustl.edu
Class: PCR with specific primers.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Pan troglodytes"
                                                                                                                                                                                                                           Nature 434 (7034), 724-731 (2005)
15815621
Contact: Joanne Nelson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 ATGCTGGTGTGCTGCACCCATTAACTC 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Volik SV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hominidae; Homo.
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ORGANISM
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BZ610242
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KEYWORDS
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                                                                                                                                                                                                                                                                                         Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou.Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp), URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·;
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AC105347Chiol_tc100.bl Chimpanzee genomic DNA Pan troglodytes
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.
1 (bases 1 to 712)
Hillier, L. W., Graves, T.A., Fulton, R.S., Fulton, L.A., Pepin, K.H.,
Minx, P., Wagner-McPherson, C., Layman, D., Wylie, K., Sekhon, M.,
Becker, M. C., Fewell, G.A., Delehaunty, K.D., Miner, T.L., Nash, W.E.,
Kremitzki, C., Oddy, L., Du, H., Sun, H., Bradshaw-Cordum, H., Ali, J.,
                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                           Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                         Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31; Indels
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Pred. No. 2.6e-07;
0; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Pan troglodytes"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomic, genomic survey sequence.
C2179389
C2179389.1 GI:58347682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic_DNA"
/db_xref="taxon:9598"
/clone="PTB-130G10.F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pan troglodytes (chimpanzee)
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R.Site 1 : SacI
R.Site 2 : SacI.
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78.9%;
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                                                                                                                                                                                                        (bases 1 to 661)
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  troglodytes
                                                                  Hominidae; Pan.
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Best Local Similarity
Matches 116; Conserv
                                                                                                                                                                                   Unpublished
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ORGANISM
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CZ179389/c
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AUTHORS
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Gaps

608

Gaps

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/mol type="mRNN" saprems
/db xref="taxon:9606"
/db xref="taxon:9606"
/db xref="taxon:9606"
/db xref="taxon:9606"
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/clone_lib="NNL010"
/note="Organ: nervous normal; Vector: pucl8; Site_l: Smal; Site_l: Smal; A mini—library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUCl8 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                             238 bp mRNA linear EST 22-JAN-2001
BF954789.
BF954789.1 GI:12372064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l (bases i tro.138)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpsonoludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM3&t2=FM3-NN1203-151100-001-d08&t5=2000-11-15&t=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                    549 GGTACATGTGCACAATGTGCAGGTTAGTTACATATGTATACATGTGCCATGCTGGTGGGG
                                                                                                                               27 IGATGATITIAATAAAATAICAITITICITITITITIAITAITATAATACITITIAAGITITIAG
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVNY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMvSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CR597534 995 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DG007YE23 of B cells (Ramos cell line) of
                                                                                                                                                                                                                                        /note="Vector: pECBAC1; Site_1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 AGTITTAGGGTACATGTGCACAATGTGCAGGTTAGTTACATATGTATACATGTGCCATGC 122
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                             /clone="MCF7]-23G10"
/sex="female"
/clone lib="Human MCF7 breast cancer cell line library
(MCF7_1)"
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/db_xref="taxon.9606"
/db_xref="taxon.9606"
/clone="cSODG007yE23"
/tissue_type="B_cells (Ramos cell line)"
/plasmid="pCMVSPORT_6"
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                                                                                                                                                                                                                                                                                                                                                                          13.9%; Score 97.4; DB 12;
84.6%; Pred. No. 2.6e-07;
ive 0; Mismatches 21;
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                                                                                                          /mol_type="genomic_DNA"
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67 CTTTAAGTTTTAGGGTACATGTGCACAATGTGCAGGTTTGTTACATATGTATACATGTGC 126
                                                                          127 CATGTTGGTGTGCTGCACCCATTAACTC 154
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                                                                                                                                                           completed: July 19, 2006, 09:20:55
ne : 4416 secs
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

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CDNA Library Preparation: Life Technologies, Inc.

CLOR distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G. E. Consortium/LLNL at:

WWW-bio.llnl.gov/bbrp/image/image.html

Insert Length: 379 Std Error: 0.00

Seg primer: -40UP from Gibco

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                                                                                                                                                    /tissue type="poorly differentiated adenocarcinoma with signet ring cell features" hab host="OHIOB" / Tab host="DHIOB" / Tab host="DHIOB" / CAP Gas4" / Note="Organ: Stomach; Vector: pCMV-SPORT6; Site 1: Sall; Stre 2: Notl; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 256)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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Pred. No. 3e-07;
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    Pred. No. 3e-07;
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